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TITLE	Molecular cloning and characterization of a murine pre-B-cell growth-stimulating factor/stromal cell-derived factor 1 receptor, a murine homolog of the human immunodeficiency virus 1 entry coreceptor fusin
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 93 (25), 14726-14729 (1996)
MEDLINE	97121456
REFERENCE	2 (bases 1 to 1877)
AUTHORS	Nagasawa, T.T.
TITLE	Molecular cloning of murine PBSF/SDF-1 receptor
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 1877)
AUTHORS	Nagasawa, T.
TITLE	Direct Submission
JOURNAL	Submitted (05-SEP-1996) Takashi Nagasawa, Research Institute, Osaka Medical Center, Department of Immunology, Muradocho 840, Izumi, Osaka 590-02, Japan (E-mail: immunol@osk.threewebnet.or.jp, Tel:0725-56-1220, Fax:0725-57-3021)

FEATURES	Location/Qualifiers
source	1. .1877

gene	1. .1877
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469 a
BASE COUNT

Query Match	100.0%	Score 1877;	DB 10;	Length 1877;
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Matches 1877;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db	1801	TATTACATTTGTTAATAAAGTCAATGATTAACCTTAAAAAaaaaaaaaaaaaaaaaaaaaaa	1860
Oy	1861	AAAAAAAAAAAAAAAAAAAA 1877	
Db	1861	AAAAAAAAAAAAAAAAAAAA 1877	

RESULT 2				
LOCUS	BC031665	1817 bp	mRNA	linear
DEFINITION	Mus musculus, chemokine (C-X-C) receptor 4, clone MGC:35266			
IMAGE:	J3592479, mRNA, complete cds.			
ACCESSION	BC031665			
VERSION	BC031665.1	GI:21618781		
KEYWORDS	MGC.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			

REFERENCE
AUTHORS
TITLE
JOURNAL

REMARK	COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov	Contact: MGC help desk

Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amgdhcm.tmc.edu
Günatiner, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Hale, S.M., yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 61 Row: 4 Column: 24
 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity, but not identity to protein.

FEATURES	Location/Qualifiers
source	1. .1817

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			Indels	1
			Gaps	1

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[illegible]

homologue of the human HIV-1 entry cofactor fusin

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3770)
AUTHORS Moeppps, B.
JOURNAL Direct Submission
Submitted (19-JUL-1996) B. Moeppps, Universitaet Ulm,
Pharmacology/Toxicology, Albert-Einstein Allee 11, D-89081 Ulm, FRG
REMARK 3 (bases 1 to 3770)
REFERENCE Revised by [3]
AUTHORS Moeppps, B.
JOURNAL Direct Submission
Submitted (02-APR-1997) B. Moeppps, Universitaet Ulm,
Pharmacology/Toxicology, Albert-Einstein Allee 11, D-89081 Ulm, FRG
COMMENT On Apr 3, 1997 this sequence version replaced gi:166646.
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DB 3426 TTTACATTTTCCAGATATAGAGAGTCAAGCTCTTGAACGTTTTTTTTTTTTTTTT 3485
QY 1313 TTAATGACTGTTGGAGATTATGTTCTCTACTTTTGTGAGTTTGAATTAATTA 1372
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Oy		1428	CCAGGTCCTTGATGACGTGGTATTATCGTGTGTAGACACTGTAAACGTGTAGAGAAGAACT	1487
Dd		3606	CCAAGTTCTTAGTAGAGCTGTTTATCTGTGTGTAGAGCACTGTAAACGTGTAGAGAAGAACT	3665
Oy		1488	GAACATTCACAAGAACTGTGTGAATTAATGAATAAGCTAGCCGTGATCCCTCAGCTGTGCTG	1547
Dd		3666	GAACATTCACAAGAACTGTGTGAATTAATGAATAAGCTAGCCGTGATCCCTCAGCTGTGCTG	3725
Oy		1548	CATATATCTCTTCATTTCCGAGAGACACCACCCCACC	1586
Dd		3726	CATATATCTCTTCATTTCCGAGAGACACCACCCCACC	3764
RESULT 6				
MU059760				
LOCUS	MU059760	1223 bp	mRNA	linear
DEFINITION	Mus musculus fusin homolog mRNA, complete cds.			ROD 09-SEP-1996
ACCESSION	U59760			
VERSION	U59760.1	GI:1527134		
KEYWORDS				
ORGANISM	Mus musculus.			
SOURCE	Mus musculus.			
REFERENCE	Heesen,M., Berman,M.A., Gerard,C. and Dorf,M.E.			
AUTHORS	Heszen,M., Berman,M.A., Gerard,C. and Dorf,M.E.			
TITLE	Cloning of the mouse homologue of the human HIV co-factor gene, fusin			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 1223)			
AUTHORS	Heesen,M., Berman,M.A., Gerard,C. and Dorf,M.E.			
TITLE	Direct Submission			
JOURNAL	Submitted (02-JUN-1996) Pathology, Harvard Medical School, 200 Longwood Avenue, Boston, MA 02115, USA			
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	BASE COUNT	285 a	342 c	268 g 328 t
ORIGIN				
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Best Local Similarity	99.7%;	Pred. No. 6.6e-242;		
Matches 1219;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
Oy		91	ACCACACGCGCTGTAGACGAGTGTGCCATGGAACCATAGTGTAGTATATACACT	150
Dd		1	ACCACACGCGCTGTAGACGAGTGTGCCATGGAACCATAGTGTAGTATATACACT	60
Oy		151	CTGATTAATCTCTGGAAGAAGTGGGGTGTGAGACTATGACATCCAACAGAAGACCTGCT	210
Dd		61	CTGATTAATCTCTGGAAGAAGTGGGGTGTGAGACTATGACATCCAACAGAAGACCTGCT	120
Oy		211	TCCGGGATGAAGACGTCATTTCAATAGACTTCTCCGCCACATCTACTTCACTATCT	270
Dd		121	TCCGGGATGAAGACGTCATTTCAATAGACTTCTCTCCGCCACATCTACTTCACTATCT	180
Oy		271	TCTTGACTGCATAGTGGCAATGAGATTGTGATCTCGTATCGGCTTACGAGAAGAAC	330

[illegible]

MLMCR13	MLMCR13	1422 bp	DNA	linear	ROD 31-OCT-1996
LOCUS	Mus musculus lcr-1 gene, exon 2.				
DEFINITION	Mus musculus lcr-1 gene, exon 2.				
ACCESSION	280113				
VERSION	280113.1	GI:1655638			
KEYWORDS	CXC chemokine receptor 4; CXCR-4; lcr-1 gene.				
SOURCE	Mus musculus.				
ORGANISM	Mus musculus.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 1422)				
TITLE	Schubel, A., Burgstahler, R. and Lippe, M.				
JOURNAL	The mouse homologue of the human HIV coreceptor CXCR-4 (FUSIN): High expression in thymus and lymphoid tissues				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 1422)				
TITLE	Lippe, M.				
JOURNAL	Submitted (11-SEP-1996) Martin Lippe, Max-Debruecker-Center for Molecular Medicine, MDC, Robert-Roesle-Strasse 10, BERLIN-BUCH, D-13122, GERMANY				
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361	ACCTGTACGTGGCTACCTCTCTTTGTCATCACATCCCTTGTGGCAGTTGATGCCA	420			
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421	TGGCTGATCGTGGTACTTTGGGAAATTTGTGTGAAGCGTGCATCTACATACATGCA	480			
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[illegible]

Molecular Medicine, MDC, Robert-Roessle-Strasse 10, Berlin-BUCH,
D-13122, GERMANY
On Nov 21, 1997 this sequence version replaced gi:1542888.
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Best Local Similarity 99.1%; Pred. No. 1.1e-226;
Matches 1160; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

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QY 196 ACAAGAACCCCTCCCGGAGTGAAGAAAGTCCATTCAATAGAGATCTTCGCCACCA 255
DB 71 ACAGAGAACCCCTCCCGGAGTGAAGAAAGTCCATTCAATAGAGATCTTCGCCACCA 130
QY 256 TCTACTTCATCATCTTCTGACTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 315
DB 131 TCTACTTCATCATCTTCTGACTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 190
QY 316 GTTACAGAAAGAGTGAAGAGATGAGGACAAAGTACCGGGTGCACCTGTGAGTGGTG 375
DB 191 GTTACAGAAAGAGTGAAGAGATGAGGACAAAGTACCGGGTGCACCTGTGAGTGGTG 250
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DB 251 ACCCTCTCTTGTGATCAGACCTCCCTCTGGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 310
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QY 556 GTCAAGGCAAGAAAGTGTGGTGAAGAAAGCACTGTATGTGGGCGTGGATCCGAG 615
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DB 491 CCCTCTCTGACTATACCTGACTTCTTGTGCGAGCTCAAGCCAGGGGAGACATGAGTC 550
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RESULT 9
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LOCUS Mus musculus fusin (CXCR-4) gene, complete cds.
DEFINITION U65580
ACCESSION U65580.1 GI:1731650
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 3366)
Heesen, M., Berman, M.A., Benson, J.D., Gerard, C. and Dorf, M.E.
Cloning of the mouse fusin gene, homologue to a human HIV-1
co-factor
J. Immunol. 157 (12), 5455-5460 (1996)
MEDLINE
J9113334
PUBMED
8955194
REFERENCE
2 (bases 1 to 3366)
Heesen, M., Berman, M.A., Gerard, C. and Dorf, M.E.
Direct Submission
TITLE
JOURNAL
Submitted (30-JUL-1996) Pathology, Harvard Medical School, 200
Longwood Avenue, Boston, MA 02115, USA
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Location/Qualifiers


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Best local similarity 98.6%; Pred. No. 2.5e-208;
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LOCUS      AR015970      Sequence 3 from patent US 5776457.
DEFINITION      AR015970
ACCESSION      AR015970
VERSION      AR015970.1 GI:3972247
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1. (bases 1 to 1737)
AUTHORS      Lee,J. and Wood,W.I.
TITLES      Antibodies to human PFA4 receptor and compositions thereof
JOURNAL      Patent: US 5776457-A 3 07-JUL-1998;
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source      1..1737
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Best local similarity 76.1%; Pred. No. 1.2e-191;
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DB      110 GAGTGTGCGCATGGAACCATGATGATGTATATACCTTGTGATTAATCTACTGTGAAGA 169
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DB      80 CAGCGGTATCAATGAG- - - - -GGGATGATGATATATACCTTGTGATTAATCTACTGAGGA 134
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Db	80	CAGGGGTTACCATGGA-----GGGATGAGTATATATACATTGAGATTAACATGACCGAAGGA	134
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QY	230	TTTCAATATAGANCTCTCCGCCACCACATCTACTTCATCATCTTCTTACHTGGCATAGTCGG	289
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QY	290	CAATGATTTGGTATCTGGTGCATGGGTATCCAGAGAAGAGCTAAAGAGCATGACGGACAA	349
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QY	350	GTACGGGCTGCACCTGTCAGTGGCTGACCTCTTGTTCATCACACTCCCTTCTGGGC	409
Db	315	GTACAGGCTGCACCTGTCAGTGGCGACCTCTTGTTCATCACACTCCCTTCTGGGC	374
QY	410	AGTTATGCGACGCTGCTGCTACTTTGGGAAATTTTGTGTGAAGGCTGCATATCAT	469
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QY	650	CGAGCTCAGCCAGGGGAGCATAGTCAGGGGGATGACAGGTATACATGTCAGCCGCTTA	709
Db	615	CAGC-----TCAGTGAAGCAGATGACAAATATATGTGTGACCGCTTCTA	659
QY	710	CCCCGATAGCCTGTGATGGTGGTGTTCATTCACAGCATATATAGTGGGCTCTACCT	769
Db	660	CCCCGATAGCTGTGGGTGGTGTGTGTTCAGATTTCCAGCAATCATGTTGGGCTTATCT	719
QY	770	GCCCCGATCGTCAATCTCTCTGTTCATGTCATCATCTCTAAGCTGTCAACATCCAA	829
Db	720	GCTGTGATTTGTCAATCTGTGCTGTCTATTTGCTATTAATCAATCTCCAACTGTCAACATCCAA	779
QY	830	GGGGCCACCAAGAGCCCAAGGCCCTCAAGAGCAGACATCTCATCTGATCTTCTTTCG	889
Db	780	GGGGCCACCAAGAGCCCAAGGCCCTCAAGAGCAGACATCTCATCTGATCTTCTTTCG	839
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QY	1070	AAGCTCTGCCAGCATATGACTCAATCCATGAGACAGAGCTCCAGGCTCAAGATCTTTC	1120
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QY	1130	CAAGAGAAAGCGGGGTGACACTCTTTCGCTTCACAGGATCGAAATCTCCAGTTTCA	1180
Db	1080	CAAGAGAAAGCGGGGTGACACTCTTTCGCTTCACAGGATCGAAATCTCCAGTTTCA	1130
QY	1190	CTCCAGCTTACCCCTTATGCAAGAGCTTATATATATATATATATATGATAAGAACTT	1240

Db	1140	CTCCAGCTAA-----CACAGATGTAAAGACTTTTTTTTATTACGATAAATACCTTT	1191			
Oy	1260	TTTATATGTTACACATTTTTCAGATATAAGAGACTGACCAGTCTTGTAACAGTTTTTTTTT	1309			
Db	1192	TTTTAAGTTACACATTTTTCAGATATAAAGAGACTGACCACAATATGTACAGTTTTTATGTC	1251			
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Oy	1370	ATATAAATATGTTTGTGTTTGTGTTTTCATGTGAANAGCCCTGAGCAGCACTGTGGCC	1429			
Db	1306	TTTATA-----TAATTTTTTTTTTTGTTTCAATATGATGTGTCTGAGCAGCACTGTGGCC	1361			
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ACCESSION	AR070433					
VERSION	AR070433.1	GI:7221321				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1737)					
AUTHORS	Lee,J. and Wood,W.I.					
TITLE	Nucleic acid encoding PFA4 receptor					
JOURNAL	Patent: US 5892017-A 3 06-Apr-1999;					
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Matches 191: Conservative 0; Mismatches 301; Indels 136; Gaps 10;						
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Db 20 GCGCGCCGAAAGTGACGCCGAGGGCTGAGTGTCTCAGTAGACCAAGCCATCTGAGAAC 79
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Qy 1850 AA 1877
Db 1684 AA 1711

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DEFINITION Sequence 3 from patent US 6087475.
ACCESSION ARI03430
VERSION ARI03430.1 GI:12815018
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1737)
AUTHORS Lee,J. and Wood,W.I.
TITLE PFAA receptor
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Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

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Best Local Similarity	76.1%	Pred. No. 1.2e-191			
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QY	110	GAGTGTGCGCATGCAACCGATCAGTGTGATATATACATCTTGTATACCTACTGTAGAG	169		
DB	80	CAGCGGTATACATGGA-----GGGATCAGTATATATACCTTCCAGTATACAGCCAGCA	134		
QY	170	AGTGGGCTGTGAGACTATGACTCCAAAGAAACCCCTGTCGGATGAAAACGTCCA	229		
DB	135	AATGGGCTCAGGGAGCTATGACTCCATGAAAGAACCCCTGTTCCGTGAAGAAATCTCTA	194		
QY	230	TTTCAATAGGATCTTCTGCGCCACCATCTACTATCATCTTCTTACGTGCAATCTCGG	289		
DB	195	TTTCAATAAATCTTCTGCGCCACCATCTACTATCATCTTCTTACGTGCAATCTCGG	254		
QY	290	CAATGATTTGTGATCTGCTGATGCTTACAGAAAGCTTAAGAGCATGAGACAGCA	349		
DB	255	CAATGATTTGTGATCTGCTGATGCTTACAGAAAGCTTAAGAGCATGAGACAGCA	314		
QY	350	GTAACGGCTGACCTCTCAGTGTGACTCTCTTTGTATCACAACCTCCCTTGTGGC	409		
DB	315	GTAACGGCTGACCTCTCAGTGTGACTCTCTTTGTATCACAACCTCCCTTGTGGC	374		
QY	410	AGTGTATGCGATGCTGATGCTTGTGGAATTTTGTGAAAGCTGCTGATCAT	469		
DB	375	AGTGTATGCGATGCTGATGCTTGTGGAATTTTGTGAAAGCTGCTGATCAT	434		
QY	470	CTACATGTCACCTCTACAGACGCTTCTCATCTGCGCTTCATGACCTGAGCCGCA	529		
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QY	530	CCATGCGATTTGTCCACGCCACCAAGCTTAAGAGCCCAAGAACTGCTGGTGAAGGC	589		
DB	495	CCATGCGATTTGTCCACGCCACCAAGCTTAAGAGCCCAAGAACTGCTGGTGAAGGC	554		
QY	590	AGTCTATGTTGGGCTGTGATGCTCCAGCCCTCTCTGATATACGATGCTGATCTTGC	649		
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QY	710	CCCCATAGCTGTGATGCTGCTTTCATTTCCAGCATATATAGTGGTCTATCCT	769		
DB	660	CCCCATAGCTGTGATGCTGCTTTCATTTCCAGCATATATAGTGGTCTATCCT	719		
QY	770	GGCGGATGCTGATCTCTGCTGTGATGATCATCTCTCAACCTGTACAGCTGCA	829		
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QY	1190	CTTCAGCTTACCCCTTATGCAAGACATATATATATATATATATATATATATATAT	1249		
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 VERSION 124455.1 GI:1604325
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 ORGANISM Unknown.
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 AUTHORS Chundharapal, A., Lee, J., Hebert, C. and Kim, K. Jin.
 TITLE Antibodies to human IL-8 type A receptor
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Db 780 GGGCCACCAAGAGCGCAGGCTCAAGACGATCTCTATCTTCTTCTTTC 839

QY 890 CTGCTGGCTGCAATATATGTGGGATGACGATGATCTCTTCTTTCGAGTCA 949
   || || || || || || || || || || || || || || || || || || || || ||
Db 840 CTGCTGGCTGCAATATATGTGGGATGACGATGATCTCTTCTTTCGAGTCA 899

QY 950 CAAGCAAGATGTACTGTGAGAGATGTGCAAGTGTATCTCATCAGAGGCGCT 1009
   || || || || || || || || || || || || || || || || || || || || ||
Db 900 CAAGCAAGATGTACTGTGAGAGATGTGCAAGTGTATCTCATCAGAGGCGCT 959

QY 1010 CGCTTCTTCTGACTGTGTGCTGAACCCCATCTTATGCTTCTGCGGCGCAAGTTCAA 1069
   || || || || || || || || || || || || || || || || || || || || ||

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Db 960 ACCTTCTTCCAGTGTGTGTGAACCCCATCTTATGCTTCTTGTGAGCCAAATTTAA 1019

QY 1070 AAGCTCTGCCAGCATGACCTCAACCTCATGAGAGGCTCCAGCTCAATCTTTC 1129
   || || || || || || || || || || || || || || || || || || || || ||
Db 1020 AAGCTCTGCCAGCATGACCTCAACCTCATGAGAGGCTCCAGCTCAATCTTTC 1079

QY 1130 CAAGGAAAGCGGCTGTGACACTCTTCCGTCCTCCAGGAGTGTGAGATCTCAGTTTCA 1189
   || || || || || || || || || || || || || || || || || || || || ||
Db 1080 CAAGGAAAGCGGCTGTGACACTCTTCCGTCCTCCAGGAGTGTGAGATCTCAGTTTCA 1139

QY 1190 CTCAGCTAACCTTATGCAAGACTTATATATATATATATATATATATATATATAT 1249
   || || || || || || || || || || || || || || || || || || || || ||
Db 1140 CTCAGCTAACCTTATGCAAGACTTATATATATATATATATATATATATATATAT 1191

QY 1250 TTTTATGTATACATTTTCCAGATATAGAGACTACAGCTCTTGTACAGTTTTC 1309
   || || || || || || || || || || || || || || || || || || || || ||
Db 1192 TTTTATGTATACATTTTCCAGATATAGAGACTACAGCTCTTGTACAGTTTTC 1251

QY 1310 TTTTATGTATGAGCTGTGAGGATTTAGTTCCTCTGCTTGTGAGGTTGACTTAAT 1369
   || || || || || || || || || || || || || || || || || || || || ||
Db 1252 TTTTATGTATGAGCTGTGAGGATTTAGTTCCTCTGCTTGTGAGGTTGACTTAAT 1305

QY 1370 ATATAAATATTTGTTTTGTTTTGTTTCAATGATGAGCTGTAGCAGAGACTGTGCC 1429
   || || || || || || || || || || || || || || || || || || || || ||
Db 1306 ATATAAATATTTGTTTTGTTTTGTTTCAATGATGAGCTGTAGCAGAGACTGTGCC 1361

QY 1430 AAGTCTTATGAGCTGTATATCTGTGTGATGAGACTGTAGAGAGAGAACTGTA 1489
   || || || || || || || || || || || || || || || || || || || || ||
Db 1362 AAGTCTTATGAGCTGTATATCTGTGTGATGAGACTGTAGAGAGAGAACTGTA 1413

QY 1490 ACATTCAGAAATGTGTGTAATTTGAATTAACCTAGCCGTGATCTGCTGCTGCA 1549
   || || || || || || || || || || || || || || || || || || || || ||
Db 1414 ACATTCAGAAATGTGTGTAATTTGAATTAACCTAGCCGTGATCTGCTGCTGCA 1473

QY 1550 TAATCTTCTCATTTCCAGAGACACCCACCCACCCACCCACCCACCCATTTAAT 1609
   || || || || || || || || || || || || || || || || || || || || ||
Db 1474 TAATCTTCTCATTTCCAGAGACACCCACCCACCCACCCACCCACCCATTTAAT 1488

QY 1610 TGTGTGTTATGCTGTGATGATGTTGTTGTTTTTGTGTTGTTGTTGTTT 1669
   || || || || || || || || || || || || || || || || || || || || ||
Db 1489 TGTGTGTTATGCTGTGATGATGTTGTTGTTTTTGTGTTGTTGTTGTTT 1525

QY 1670 TTTTCTGTAAAGATGCACTTAAACCAAGCCTGAAGTGTGTAAGTCTGGGCT 1729
   || || || || || || || || || || || || || || || || || || || || ||
Db 1526 TTTTCTGTAAAGATGCACTTAAACCAAGCCTGAAGTGTGTAAGTCTGGGCT 1581

QY 1730 TTTTCTGTGTTGTTGTTTTCAGTTTCAAGAGTATGATTAATCTGCTTCAAT 1789
   || || || || || || || || || || || || || || || || || || || || ||
Db 1582 TTTTCTGTGTTGTTGTTTTCAGTTTCAAGAGTATGATTAATCTGCTTCAAT 1623

QY 1790 GTACAGCTCTGTATTTACATTTGTTAATAAAGCATGATAAATCTTAAAAA 1849
   || || || || || || || || || || || || || || || || || || || || ||
Db 1624 GTACAGCTCTGTATTTAAGTTTAAATAAAGTACATGTTAACTTAAAAA 1683

QY 1850 AAAAAAAAAAAAAAAAAAAAAAAAAA 1877
   || || || || || || || || || || || || || || || || || || || || ||
Db 1684 AAAAAAAAAAAAAAAAAAAAAAAAAA 1711

```

Search completed: July 12, 2003, 15:58:37
 Job time : 3312 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 14:05:23 ; Search time 1852 Seconds
(without alignments)
16414.108 Million cell updates/sec

Title: US-09-367-052-1

Perfect score: 1877

Sequence: 1 ccacccaatacagactcact.....aaaaaaaaaaaaaaaaaaaa 1877

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Search: 16154066 seqs, 8097743376 residues

Number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_ges:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	684.8	36.5	1051	13	BM545259 AGENCOURT
2	631.4	33.6	958	12	BG174412 602334232
3	621.6	33.1	793	9	AA182270 mt83f01.r
4	621.2	33.1	639	9	AA1816049 vr14h02.r
5	610.2	32.5	753	13	BG915636 602814106
6	594	31.6	910	13	B1762229 603049139

7	590	31.4	955	12	BG173867
8	578.4	30.8	891	13	B1824663
9	576.8	30.7	950	14	B0718617
10	576.2	30.7	628	10	AM227957
11	576	30.7	904	12	BF100790
12	558	29.7	1034	14	BM920800
13	552.8	29.5	765	13	BM387369
14	551.6	29.4	582	12	BG145042
15	547.4	29.2	827	13	B1761664
16	524.8	28.0	528	12	B6277031
17	524.8	28.0	750	12	BG217352
18	520.4	27.7	875	13	B1756157
19	511.4	27.2	585	10	BE627479
20	509.6	27.1	913	13	BM051973
21	509	27.1	886	12	BF101953
22	495.8	26.4	746	13	B1917014
23	492.6	26.2	905	13	B1754094
24	484.2	25.8	782	12	BG685901
25	481.6	25.7	728	9	AU117058
26	479	25.5	846	12	BF338608
27	478.2	25.5	702	13	B1761118
28	472.4	25.2	514	12	BG093377
29	470.4	25.1	680	14	BQ109515
30	468.4	25.0	742	13	B1597875
31	464.2	24.7	952	13	B1821693
32	463	24.7	703	13	B1765768
33	453.2	24.1	658	13	B1835125
34	447.8	23.9	917	12	BE872980
35	443.2	23.6	645	9	A1884548
36	441	23.5	510	9	AA190052
37	440.8	23.5	858	12	BF979340
38	439.4	23.4	553	12	BG145062
39	438.8	23.4	512	12	BF720603
40	435.8	23.2	671	12	BG025793
41	426	22.7	437	12	BG093470
42	423.2	22.5	748	13	B1546999
43	418	22.3	446	9	A1131863
44	411.8	21.9	484	9	AA120018
45	410.6	21.9	561	12	BF591285

ALIGNMENTS

RESULT 1
LOCUS BM545259 1051 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6497171 NIH_MGC_124 Homo sapiens CDNA clone IMAGE:5726963
ACCESSION BM545259
VERSION BM545259.1 GI:18777197
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1051)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Place: LLNL12720 row: e column: 12
High quality sequence start: 20
High quality sequence stop: 753.
Location/Qualifiers

FEATURES

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source
1. 1051
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5726963"
/clone_lib="NIH_MGC_124"
/tissue_type="hippocampus"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMV-Sport6; Site: 1; EcoRV
(destroyed); Site: 2; NotI; RNA source: male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

BASE COUNT      240 a      302 c      238 g      271 t
ORIGIN

Query Match      36.5%; Score 684.8; DB 13; Length 1051;
Best Local Similarity 81.6%; Pred. No. 2.5e-73;
Matches 873; Conservative 0; Mismatches 172; Indels 25; Gaps 6;

54 GTAGAGAGGACCCCTGAGGCGCTTGCGTCCGGTACCCAGGCGGTAGAGCACT 113
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 GTAGCAAGGTGACGCCGAGGCTGTCTGCTCAGTACGCCGATCGAGAACAGC 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
114 GTTGCCATGGAACCCATGATGTGATATATACCTTGTGATACCTGTAAGAGTG 173
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 GGTTCACATGGA-----GGGATCAGTATATACCTTCAGATACACCGAGGAATG 115
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
174 GGGTTCGAGACTATGATGATCACAAGAACCCCTTCGGGATGAAAACGCTATTTC 233
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
116 GCTTCAGGSGATATAGACTCCATGGAAGAACCCCTTCCGTAAGAAATGCTAATTTC 175
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
234 AATAGACTCTTCCTGCCCCACCATCTACTTATCATCTCTTGACAGATAGCGCAAT 293
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
176 AATAAATCTTCTCTCCACCATCTACTTCACTTCTTAACTGGATGTGGCAAT 235
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
294 GATTGTGATCCTGCTGATGGGTACAGAGAAGTAAAGAGCATGACGACAAAGTAC 353
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
236 GGATTGGTATCCTGTGTCATGGGTACAGAGAAGTAAAGTAAAGTACGACAAAGTAC 295
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
354 CGGTCGACCTGTCACTGCTGCTCTCTTGTATCAGTACCTCCCTTCTGGGCACTT 413
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
236 AGGCTGACACTGTGCTGCTGCTCTCTTGTATCAGTACCTCCCTTCTGGGCACTT 355
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
414 GATGCTAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 473
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
356 GATGCTAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 415
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
474 ACTGTCAACCTTACAGAGGCTTCTCATCTGCTGCTTCACTAGGCTGACCGGTACTC 533
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
416 ACAGTCAACCTTACAGAGGCTTCTCATCTGCTGCTTCACTAGGCTGACCGGTACTC 475
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
534 GCCATTGTCCAGCCACCAAGTAAAGGCCAAGAAAGTCTGCTGCTGCTGCTGCTGCTG 593
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
476 GCCATGTCTCAGCCACCAAGTAAAGGCCAAGAAAGTCTGCTGCTGCTGCTGCTGCTG 535
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
594 TATGTGGGCGTGTGATCCAGGCTTCTCATCTGCTGCTTCACTAGGCTGACCGGTACTC 653
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
536 TATGTGGGCGTGTGATCCAGGCTTCTCATCTGCTGCTTCACTAGGCTGACCGGTACTC 595
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
654 GTACAGCCAGGCGGATCAGTACAGGCGGATGACAGTATCTGTGACCGCTTATACCCG 713
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
596 G-----TCAGTAGGCGATGACATATATCTGTGACCGCTTATACCCG 640
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
714 GATACCTGTGATGCTGTGCTTCAATTCAGCATATATGCTGGTCTCATCTGCTGCTG 773
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
641 AATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 700
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
774 GGCATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 833
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
701 GGTATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 760
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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834 CACGAGAGCCGCAAGCCCTCAAGACGACATCATCTCATCTTCTTCTTCTGCTGC 893
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
761 CACGAGAGCCGCAAGCCCTCAAGACGACATCATCTCATCTTCTTCTTCTGCTGC 820
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
894 TGGCTGCATATATATGTGGGATGACATGATGATCTCTTCTCTTCTTGGGATCATCAAG 953
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
821 TGGCTGCATATATATGTGGGATGACATGATGATCTCTTCTCTTCTTGGGATCATCAAG 880
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
954 CAA-GGATGTACTTCGAGACATGTTGCAAGGATGCAAGGATGCAAGGATGCAAGGATGCAAG 1011
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
861 CAAGGCGGTGATGTTGAGAACACGCTGACAGATGATGATGATGATGATGATGATGATGATG 940
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1012 CTTTCTTCACTGTTTGGCTGAACCCCATCTTATGCTT--CTCGGGGCCCAAGTTCA 1069
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
941 CTTTCTTCACTGTTTGGCTGAACCCCATCTTATGCTTCTTCTTGGGATCATCAAG 1000
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1070 AAGCTTCCGCAAGCATGCACTCACTCATG-AGCAGAGGCTCCAGCCTC 1118
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1001 AACCTTGGCCAGACGACATCTCTGTGTAACAAAGGCTGAGCCTC 1050
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
BG174412      958 bp      mRNA      linear      EST 06-FEB-2001
LOCUS      602334232P1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4457694 5',
DEFINITION      mRNA sequence.
ACCESSION      BG174412
VERSION      BG174412.1 GI:12681115
KEYWORDS      EST.
SOURCE      house mouse.
ORGANISM      Mus musculus.
REFERENCE      NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL      Contact: Robert Strausberg, Ph.D.
COMMENT      Email: cga@bbs.femail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LLM10254 row: O column: 07
High quality sequence stop: 628.
Location/Qualifiers
1. 958
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4457694"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-Sport6; Site: 1; SalI;
Site: 2; NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT      227 a      266 c      266 g      199 t
ORIGIN

Query Match      33.6%; Score 631.4; DB 12; Length 958;
Best Local Similarity 96.2%; Pred. No. 6.5e-67;
Matches 690; Conservative 0; Mismatches 21; Indels 6; Gaps 4;

54 GTAGAGTACCCCTCTGAGGCGTTTGGTCCGGTAAACCAACGAGGCTGTAGAGCACT 113
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 GTAGAGTACCCCTCTGAGGCGTTTGGTCCGGTAAACCAACGAGGCTGTAGAGCACT 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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OY	-	114	GTTGGCATTGGAACCCATAGTGTGATGATTAACAACCTTGCGATAACTACTCGAAGAAGTC	173
Dd		61	GTTGCCATTGNAACCAGATCAGTGTGATGATTAACAACCTTGCGATAACTACTCGAAGAAGTC	120
OY		174	GGGCTGTGAGACTATGACTATGCACAAAGAACCCCTGCTCCGGGATGAAGAAACGTCATTTC	233
Dd		121	GGGCTGTGAGACTATGACTATGCACAAAGAACCCCTGCTCCGGGATGAAGAAACGTCATTTC	180
OY		234	AATAGGATCTTCTGCCCCACCATCTACTTTCATCATCTTCTTGACTGGCAATAGTCGGCAAT	293
Dd		181	AATAGGATCTTCTGCCCCACCATCTACTTTCATCATCTTCTTGACTGGCAATAGTCGGCAAT	240
OY		294	GGATTGTGGATCCCTGGTCATGGGTATACCAAAGAAAGCTAAGGAGATACAGCAAGAAC	353
Dd		241	GGATTGTGGATCCCTGGTCATGGGTATACCAAAGAAAGCTAAGGAGATACAGCAAGAAC	300
OY		354	CGGCTGCACCTGTCAAGTGGCTGACCTCCTCTTGTGCATCACACTCCCTCTGGGACAGTT	413
Dd		301	CGGCTGCACCTGTCAAGTGGCTGACCTCCTCTTGTGCATCACACTCCCTCTGGGACAGTT	360
OY		414	GATGCCATNGCCTGACTGCTACTTTGGGAAATTTTGTGTAAAGCTGTCCATATCATAC	473
Dd		361	GATGCCATNGCCTGACTGCTACTTTGGGAAA--TTTTGTAAAGGCTGTCCATATCATATAC	419
OY		474	ACTGTCACCTCTACAGCAGGGTTCTACNCCGGGCTTATCAGCTGGACCGGATCCCTC	533
Dd		420	ACTGTCACCTCTTACAGCAGGGTTCTACNCCGGGCTTATCAGCTGGACCGGATCCCTC	479
OY		534	GCCATTGTGCACGCCACCACAGTCACAAAGGCCAAGAACTGCTGGCTGMAAAGGCAGTTC	593
Dd		480	GCCATTGTGCACGCCACCACAGTCACAAAGGCCAAGAACTGCTGGCTGMAAAGGCAGTTC	539
OY		594	TATGTGGGCGCTGTGATATCCAGCCCTCCTCTGACTATACCTGACTTATCTTTGCGCAG	653
Dd		540	TATGTGGGCGCTGTGATATCCAGCCCTCCTCTG--TATACCTGACTTATCTTTGCGCAG	598
OY		654	GTCAGCCAGGGGGACATCAGTCAGGGGGATGACAGTCACTCTTGAGCCGCTTAAACCC	713
Dd		599	GTCAGCCAGGGGGACATCAGTCAGGGGGATGACAGTCACTCTTGAGCCGCTTAAACCCGA	658
OY		714	GATAGCCCTGTGATGCTGTTCATATTCACAGCATATATAGTGGGTCTCATCTCTG	770
Dd		659	TA---GCTGTGATGAGGGGGCG-TTCAACTCCAGCATATAAGGGGTCATCTCTGCG	711

RESULT 3
DIS
DEFINITION
AA182270
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

793 bp mRNA linear EST 06-JAN-1997
m3f3f01.r1 Soares mouse lymph node NBMLN Mus musculus cDNA clone
IMAGE:636505 5' similar to gb.L06197 PROBABLE G PROTEIN-COUPLED
RECEPTOR LCRI HOMOLOG (HUMAN), mRNA sequence.

AA182270
AA182270.1 GI:1765810
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 793)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubouque,T.,
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

[illegible]

QY	688	GGTACATCTGTGATACCGCCTTTTCCCGGATGCGTGTGATGCTGTTCATATCCAGC	747		
Db	14	GGTACATCTGTGATACCGCCTTTTACCCGATAGGCTGTGATGCTGTTCATATCCAGC	73		
QY	748	ATAATAATGGTGGGTCTCATCTCGCCCGGACATGTCATCTCTCCGTATTACTGATCATCA	807		
Db	74	ATAATAATGGTGGGTCTCATCTCGCCCGGACATGTCATCTCTCCGTATTACTGATCATCA	133		
QY	808	TCCTCTAGTGTGTACACACTCCCAAGGGCCACACGAAGCCGACAGGCCCTCAAGACGACATCA	867		
Db	134	TCCTCTAGTGTGTACACTCCCAAGGGCCACACGAAGCCGACAGGCCCTCAAGACGACATCA	193		
QY	868	TCCTCATCTCCAGCTTTCTTTGGCTCTGCTGCTGCTGCTATATTATGTGGGATGAGCATCGACT	927		
Db	194	TCCTCATCTCCAGCTTTCTTTGGCTCTGCTGCTGCTGCTATATTATGTGGGATGAGCATCGACT	253		
QY	928	CCCTTCATCTTTTGGGAGTATCAACGAAGATGTGACTTGTGAGAGCATTTGTGCACAGT	987		
Db	254	CCCTTCATCTTTTGGGAGTATCAACGAAGATGTGACTTGTGAGAGCATTTGTGCACAGT	313		
QY	988	GGATTCATCATCAGAGGCGCTCGGCTCTTTCATCTGTGCTGCTACACCCATCCTCTATG	104		
Db	314	GGATTCATCATCAGAGGCGCTCGGCTCTTTCATCTGTGCTGCTACACCCATCCTCTATG	373		
QY	1048	CCTTCTCTGGGGGCCAAGTTCAAAGCTCTGTGCCAGCATGACACTCACTCATGAGCAGAG	110		
Db	374	CCTTCTCTGGGGGCCAAGTTCAAAGCTCTGTGCCAGCATGACACTCACTCATGAGCAGAG	433		
QY	1108	GCCTCAGCCCTCAAGATCTCTTTCCAAGGAAAGCGGGGTGGACACTCTTCGCTCCAGCG	116		
Db	434	GCCTCAGCCCTCAGAGATCTCTTTCCAAGGAAAGCGGGGTGGACACTCTTCGCTCCAGCG	493		
QY	1168	AGTCAGAAATCTCTCAGTTTCTACTCCAGCTAACCTTATGCAAGACTTATATATATAT	122		
Db	494	AGTCAGAAATCTCTCAGTTTCTACTCCAGCTAACCTTATGCAAGACTTATATATATAT	553		
QY	1228	ATATATATATGATTAAGAACTTTTATGTATACACATTTCCATATATTAAGACAGCTAGC	128		
Db	554	ATATATATATGATTAAGAAACTTTTATGTATACACATTTTCCAGTATATAGAGACTAGC	613		
QY	1288	AGCTCTGTACAGTTTTTTTTTTTTTTTTT	1313		
Db	614	AGCTCTGTACAGTTTTTTTTTTTTTTTTT	639		
RESULT 5	BG915636	753 bp	mRNA	linear	EST 05-JUN-2000
LOCUS	BG915636	602814106F1	NCI_GCAP_Mam4	Mus musculus	CDNA clone IMAGE:4936465.5
DEFINITION					mRNA sequence.
ACCESSION	BG915636				
VERSION	BG915636.1				GI:14296112
KEYWORDS					EST.
SOURCE					house mouse.
ORGANISM					Mus musculus
REFERENCE					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
AUTHORS					NIH-MGC
TITLE					http://mgc.nci.nih.gov/
JOURNAL					National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT					Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Lothar Hennighausen, Ph.D., Priscilla Furth, Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Incyte Genomics, Inc.

FEATURES
source
High quality sequence stop: 683.
Location/Qualifiers
1..753

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/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-Sport6; Site: 1: SalI; Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lotmar Hennighausen/Priscilla Furth. NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 5-11 (1996)."

BASE COUNT
175 a 204 c 189 g 185 t

Query Match
Best Local Similarity 98.1%; Pred. No. 2.7e-64;
Matches 670; Conservative 0; Mismatches 8; Indels 5; Gaps 5;

50 GCAGGTACAGTACCTCTGTGAGGGCTTGTGTCGCGTACACACAGCGCTGTAGAGC 109
10 GGAGGTACAGTACCTCTGTGAGGGCTTGTGTCGCGTACACACAGCGCTGTAGAGC 69
110 GAGTGTCCATGAGAACCGATCAGTGTAGTATACACTTGTGATCTGATCTGAGAGA 169
70 GAGTGTCCATGAGAACCGATCAGTGTAGTATACACTTGTGATCTGATCTGAGAGA 129
170 AGTGGGCTGTGAGACTGTAGACTCCACAGAGACCTCTCCGGATGANAAGCTCA 229
130 AGTGGGCTGTGAGACTGTAGACTCCACAGAGACCTCTCCGGATGANAAGCTCA 189
220 TTTCATATAGATCTTCTGCGCCACCATCTACTTTCATCTTCTGACTGGCATAGTGG 289
190 TTTCATATAGATCTTCTGCGCCACCATCTACTTTCATCTTCTGACTGGCATAGTGG 249
290 CAATGATTTGGATCGTGGTATCGATGGTTACAGANAAGCTAAGGAGATACAGGACAA 349
250 CAATGATTTGGATCGTGGTATCGATGGTTACAGANAAGCTAAGGAGATACAGGACAA 309
350 GTACCGGCTGCACCTGTAGTGGTACCTCTCTTGTGATCAGACACTCCCTCTGGGC 409
310 GTACCGGCTGCACCTGTAGTGGTACCTCTCTTGTGATCAGACACTCCCTCTGGGC 369
410 AGTGTATCCATGCTGCTGACTGTGCTTGGAAATTTTGTGTAAGGCTGTCCATATCAT 469
370 AGTGTATCCATGCTGCTGACTGTGCTTGGAAATTTTGTGTAAGGCTGTCCATATCAT 428
470 CTACACTGTCAACCTCTACAG-CAGCGTTTCTATCTGCGCTTCTATCAGCTGTGACCGGT 528
429 CTACACTGTCAACCTCTACAGCTGCTGCTTCTATCTGCGCTTCTATCAGCTGTGACCGGT 488
529 ACCTTGCCATTTGTCACGCCACCAACAGTCAAGGCCAAGAAATGCTGCTGAGAA-AG 587
489 ACCTTGCCATTTGTCACGCCACCAACAGTCAAGGCCAAGAAATGCTGCTGAGAAAG 548
588 GCAGTCTATGTGGGCTGTGATCCAGCGCTCTCTGCTGATATACCTGACTTTCATCTTT 647
549 GCAGTCTATGTGGGCTGTGATCCAGCGCTCTCTGCTGATATACCTGACTTTCATCTTT 608
648 GCCGAGTGTGAGGAGGAGATCAGTACAGG-GGATGACAGTACATCTGTGACCGCT 706
609 GCCGAGTGTGAGGAGGAGATCAGTACAGG-GGATGACAGTACATCTGTGACCGCAT 668
707 TTACCCGATAGACTGTGAGATG 729
669 TTA-CCGATAGCCTGTATATG 690

RESULT 6
BI762229
LOCUS
DEFINITION
603049139P1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5189552 5', mRNA sequence.
ACCESSION
BI762229
VERSION
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 910)
NIH-MGC <http://mhc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LAM11473 row: m column: 09
High quality sequence stop: 827.

FEATURES

source

1..910
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/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library."
BASE COUNT
210 a 260 c 208 g 232 t
ORIGIN

Query Match
Best Local Similarity 80.8%; Pred. No. 2e-62;
Matches 750; Conservative 0; Mismatches 155; Indels 23; Gaps 4;

50 GCAGGTACAGTACCTCTGTGAGGGCTTGTGTCGCGTACACACAGCGCTGTAGAGC 109
3 GCAGGTACAGTACCTCTGTGAGGGCTTGTGTCGCGTACACACAGCGCTGTAGAGC 62
110 GAGTGTCCATGAGAACCGATCAGTGTAGTATACACTTGTGATCTGATCTGAGAGA 169
63 CAGCGTTACCATGGA-----GGGATCAGTATATATACCTTGTAGATACACCGAGGA 117
170 AGTGGGCTGTGAGAGTATGACTCCACAGAGACCTCTCCGGATGANAAGCTGCA 229
118 AATGGGCTGTGAGGAGACTATGACTCATAGAGAACCTCTCTCCGTGAAGAAATGCTAA 177
230 TTTCATATAGATCTTCTGCGCCACCATCTACTTCAATCTTCTGACTGGCATAGTGG 289
178 TTTCATATAAATCTTCTGCGCCACCATCTACTTCAATCTTCTGACTGGCATAGTGG 237
290 CAATGATTTGGATCGTGGTATCGATGGTTACAGANAAGCTAAGGAGATACAGGACAA 349
238 CAATGATTTGGATCGTGGTATCGATGGTTACAGANAAGCTAAGGAGATACAGGACAA 297
350 GTACCGGCTGCACCTGTAGTGGTACCTCTCTTGTGATCAGACTCCCTCTTGTGGGC 409

Db 298 GTACAGGCTGCACCTGTGAGTGGCCGACCTCTCTTTGTCATCAGCGTTCCCTCTGGGC 357
Oy 410 AGTTATATCCATGGCTGACTGTACTTTGGGAAATTTTGTGAAGCGCTGCCATATCAT 469
Db 358 AGTTATATCCGCGCAACCTGTACTTTGGGAACTTCTATGAGGACAGTCCATGATCAT 417
Oy 470 CTACACTGTCAACCTCTACAGAGCGTTCTACTCTGCGCTTCATCAGCGTGCAGCGGTA 529
Db 418 CTACAGACTCAACCTCTACAGAGAGTGTCTCTACTCTGCGCTTCATCAGTGCAGCGTA 477
Oy 530 CCTGCGCATTTGTCCAGCGCCACACAGTCAAGGCGCAAGAAAGTCTGCTGGAAGGC 589
Db 478 CTTGGCCATTCGTCACGCGCACACACAGTCAAGGCGCAAGAGCTGTTGGCTGAAGAAGT 537
Oy 590 AGTATATGTTGGCGCTGTGATGCCAGCCCTCTCTGACTATACCTGACTCATCTTTGC 649
Db 538 GGTCTATGTGTGGCTGTGGATCCCTGCGCTCTGCTGACTATTTCCGACTTCATCTTTGC 597
Oy 650 CGACGTCAGCGCAGGCGGACATCAGTCAAGGCGGATGACAGTACATCTGTGACCGCTTTA 709
Db 598 CAACG-----TCAGTAGGCGAGATCACAGATATATCTGTGACCGCTTATCT 642
Oy 710 CCCCAGTACCTGTGATGTGTGTTTCATTCAGATATATGTTGGTCTGATCCT 769
Db 643 CCCCAGTACCTGTGATGTGTGTTTCATTCAGATATATGTTGGTCTGATCCT 702
Oy 770 GCGCGGCAATGCTATCTCTCTGTTACTGATCATCATCTCTAGCGTGCACATCCAA 829
Db 703 GCTGTGATATGCTATCTCTCTGTTACTGATCATCATCTCTAGCGTGCACATCCAA 762
Oy 830 GGGCCACCAAGAGCGCCCTCAGACAGCATCATCTCTAGCGTGCACATCCAA 888
Db 763 GGGCCACCAAGAGCGCCCTCAGACAGCATCATCTCTAGCGTGCACATCCAA 822
Oy 889 CCTGCTGCTGCATATATGTGGGATCAGCATGACT--CCTTCATCTTTTGGAGT 946
Db 823 CTTGTTGGCTGCTTACTACTTTGGGATCAGCATGATCTCTTACCTCTGGAATC 882
Oy 947 CATCAAGCAGGATGTGACTTCGAGAGC 974
Db 883 CATCAAGCAGGATGTGACTTTGAAAC 910

RESULT 7
Bg173867
LOCUS
DEFINITION Bg173867 955 bp mRNA linear EST 06-FEB-2001
602333928f1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4457119 5',
mRNA sequence.
LOCATION Bg173867
Bg173867.1 GI:12680570
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 955)
NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
COMMENT Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incey Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0253 row: g column: 08
High quality sequence stop: 652.
FEATURES
source location/Qualifiers
1..955

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/strain="FVB/N"
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/db_xref="IMAGE:4457119"
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/tissue="type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="organ: mammary; Vector: pcMV-SpOrf6; Site:1; SalI;
Site:2; NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 218 a 255 c 236 g 246 t
ORIGIN

Query Match 31.4% Score 590; DB 12; Length 955;
Best Local Similarity 90.5% Pred. No. 5.7e-62;
Matches 724; Conservative 0; Mismatches 55; Indels 21; Gaps 8;

Oy 73 GCGTTTGGTGTCCGCTAACCACACAGCGCTGAGAGCGAGTGGCCATGGAACGATCA 132
Db 1 GCGTTTGGTGTCCGCTAACCACACAGCGCTGAGAGCGAGTGGCCATGGAACGATCA 60
Oy 133 GTGTAGATATATACACTTCTGATATACCTGCTGAGAGAGTGGGCTGAGACTATGACT 192
Db 61 GTGTAGATATATACACTTCTGATATACCTGCTGAGAGAGTGGGCTGAGACTATGACT 120
Oy 193 CCACACAGAACCCCTGCTCCGGGATGAAGAGTGCATTTCAATAGATCTTCTGCCCA 252
Db 121 CCACACAGAACCCCTGCTCCGGGATGAAGAGTGCATTTCAATAGATCTTCTGCCCA 180
Oy 253 CCATCTATCTATCATCTCTTCTGACTGCGATAGTGGCAATGATTTGGTATCTCTGATCA 312
Db 181 CCATCTATCTATCATCTCTTCTGACTGCGATAGTGGCAATGATTTGGTATCTCTGATCA 240
Oy 313 TGGTTTACCAAGAGAGTAAAGAGATGAGGAGACAGTACCGGCTGACCTGTCACTGG 372
Db 241 TGGTTTACCAAGAGAGTAAAGAGATGAGGAGACAGTACCGGCTGACCTGTCACTGG 300
Oy 373 CTGACCTCTCTTGTATCATACACTCCCTCTGCGGAGTTGATGCCATGGCTGACTGGT 432
Db 241 TGGTTTACCAAGAGAGTAAAGAGATGAGGAGACAGTACCGGCTGACCTGTCACTGG 300
Oy 301 CTGACCTCTCTTGTATCATACACTCCCTCTGCGGAGTTGATGCCATGGCTGACTGGT 360
Db 301 CTGACCTCTCTTGTATCATACACTCCCTCTGCGGAGTTGATGCCATGGCTGACTGGT 360
Oy 433 -ACTTTGGGAAATTTTGTGAAGCTGTCCATATCATCTACAC--TGTCAACCTCT 486
Db 361 AACTTTGGGAAATTTTGTGAAGCTGTCCATATCATCTACAC--TGTCAACCTCT 420
Oy 487 ACAGCAGCTTCTCATCTCTGCGCTTTCATCAGCTGAGCGGTACCTGCCATTGTCACAG 546
Db 421 AGAGAGAGTGTCTCATCTCTGCGCTTTCATCAGCTGAGCGGTACCTGCCATTGTCACAG 480
Oy 547 CCACCAACAGTCAAGGCGCAAGGAAACGTGCGTGGAAAGAGAGTATATGCGGCTCT 606
Db 481 CCACCAACAGTCAAGGCGCAAGGAAACGTGCGTGGAAAGAGAGTATATGCGGCTCT 540
Oy 607 GGATGCCAGCCCTCTCTGACTATCTGACTGATCTGATCTTTCGCGA--CGTACGACGAGGG 665
Db 541 GGATGCCAGCCCTCTCTGACTATCTGACTGATCTTTCGCGA--CGTACGACGAGGG 600
Oy 666 GACATCACTGAGGGGAGTACA--GATACATCTGTGACGCGCTTTACCCGATAGCCT-- 721
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Oy 722 ----GTGATAGTGTGTTTCAATTCACGATATTA--TGTGGGCTCTATCTGCGCGC 776
Db 661 TGCAGTTGGCTGTGTTTCAATTCACGATATTA--TGTGGGCTCTATCTGCGCGC 720
Oy 777 A----TGTCAATTCGCTCTCTGATCTGATCATATCTTAAAGGTCACGATCAAGG 832
Db 721 ATTGCTCATCTCTCTCTGATCTGATCATATCTTAAAGGTCACGATCA--TCCAGGCG 779
Oy 833 CCACGAGAGCGCAAGGCGC 852

Db	780	CACCCAGAGAGCGAGCTC	799
RESULT 8			
BI824663			
LOCUS			
DEFINITION	603033815p1 NIH_MGC_115	891 bp	mRNA linear EST 04-OCT-2001
ACCESSION	BI824663		
VERSION	BI824663.1	GI:15936213	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 891)		
TOURNAL	NIH-MGC http://mgs.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.llnl.gov Plate: LM11435 row: n column: 03 High quality sequence stop: 827.		
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	/clone_lib="NIH_MGC_115"		
	/lab_host="DH10B"		
	/note="Organ: pooled brain, lung, testis; Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH-MGC Library."		
GC COUNT	207 a	250 c	205 g 229 t
GC IN			
Query Match	30.8%;	Score 578.4;	DB 13; Length 891;
Best Local Similarity	80.2%;	Pred. No. 1.5e-60;	
Matches 725;	Conservative 0;	Mismatches 156;	Indels 23; Gaps 3;
Db	70	GAGCGCTTGGTGTCCGGGTAAACCAACGCGCTGTAGAGGAGTGTCATGGAACGA	129
Y			
Db	4	GAGGGCCCTGAGTGTCTCCAGTAGCCACCCGCACTGGAGAACGCGCTTACCATGGA	59
Y	130	TCAGTGTAGTATATACACTCTCTATATACCTGAGAGAGTGGCGCTGTGACACTATG	189
Db	60	-GGGANTAGTATATATACCTCTTAACTGACATGTGGCAATGATGGTACATCTCGG	118
Y	190	ACTCCAAACGAAGAACCTGTCTCCGGGATGAAAGCTGCATTGCATATAGATCTTCCG	249
Db	119	ACTCCATTAAGAAACCTGTCTCCGGGATGAAAGCTGCATTGCATATAGATCTTCCG	178
Y	250	CCACCATCTACTATCATCTTCTTGAATGAGTGGCAATGATGGTGTGATCTCGG	309
Db	179	CCACCATCTACTATCATCTTCTTGAATGAGTGGCAATGATGGTGTGATCTCGG	238
Y	310	TCATGGTGTACCAAGAAAGCTAGAGACATAGAGGACAAAGTACCGGCTGACCTGTAG	369
Db	239	TCATGGTGTACCAAGAAAGCTAGAGACATAGAGGACAAAGTACCGGCTGACCTGTAG	298

QY	370	TGGCTGACCTCTCTTTGTGCAATCAGACACGCCCCCTTGTGGAGGTGGATGACCATTTGGCTACT	429
Db	239	TGGCCGACCTCTCTTTGTGCAATCAGACGCTCCCTTCTGTGGAGGTGGATGACCATTTGGCTACT	358
QY	430	GGTACTTTGGAAATTTTGTGTAAAGCGTGTCCATATCATCTACAGCTGTCAACCTTACA	489
Db	359	GGTACTTTGGAAATTTTGTGTAAAGCGTGTCCATATCATCTACAGCTGTGTCAACCTTACA	418
QY	490	GCAGCGTTCTATCTGTGGCTTTTCATCAGACCTTGAGACCGGTACCTTGGCATTTGTCCACGCCA	549
Db	419	GCAGCGTTCTATCTGTGGCTTTTCATCAGACCTTGAGACCGGTACCTTGGCATTTGTCCACGCCA	478
QY	550	CCACAGTCACAAAGCCCAAGAAACTGCTGGGCTGAAAAAGCGAGTGTATGTGGCGCTTGGGA	609
Db	479	CCACAGTCACAAAGCCCAAGAAACTGCTGGGCTGAAAAAGCGAGTGTATGTGGCGCTTGGGA	538
QY	610	TCCAGACCCCTCTCTGTGATATATACCTGTGACTTTCATCTTTGGCCGAGTGCAGCCAGGCGGACA	669
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QY	730	TGTGTGTTTCAATTCAGCATATATATATGAGGAGTGTGCATCTCTCCCGGATCTGTCAATCTCT	789
Db	645	TGTGTGTTTCAATTCAGCATATATATATGAGGAGTGTGCATCTCTCCCGGATCTGTCAATCTCT	704
QY	790	CTGTGTATCTGATCATCTATCTGTAAAGCTGTGCACACTCCCAAGGGCCACAGAGCGCAGAG	849
Db	705	CTGTGTATCTGATCATCTATCTGTAAAGCTGTGCACACTCCCAAGGGCCACAGAGCGCAGAG	764
QY	850	CCCTCAAGACAGACAGTCTATCTCTTACTCTCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	905
Db	765	GCCCTCAAGACAGACAGTCTATCTCTTACTCTCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT	824
QY	906	TATGTGGGATACACATGACATCTCTTCAATCTTTGGAGTGCATCAAGCAAGATGTGCAC	965
Db	825	ACATTTGGGATACACATGACATCTCTTCAATCTTTGGAGTGCATCAAGCAAGATGTGCAC	884
QY	966	TTTCG 966	
Db	885	TTTCG 888	

source

1. 765
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/strain="Sprague-Dawley"
/db.xref="taxon:10116"
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/clone_id="UI-R-CNI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pUT3D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-CNI
library is a subtracted library derived from the following
pool of seven normalized rat libraries: normalized rat
seminal vesicles, normalized rat penis, normalized rat
bladder, normalized rat cervix, normalized rat brown
adipose, normalized rat fundus, and normalized rat
salivary gland. It was constructed according to the
procedure described by Bonaldo, Lennon & Soares (Genome
Research genome 6: 791-806, 1996). For construction of
the CNI library, plasmid DNA from the pool of normalized
libraries was electroporated into competent bacteria for
the production of single-stranded circular DNA. This was
then used as a tracer in a subtractive hybridization with
a driver (PCR amplified inserts from a plasmid DNA template
preparation) comprising: a) a pool of about 34,000 clones
from the Rat Unigene Set corresponding to plates R-5-AA-NN
excluding plates R-5-MM and MN. This pool represented 40%
of the final driver population. b) a pool of about 29,000
clones from subtracted libraries CA0 and CA1 corresponding
to plates R-CA0-AMV through R-CA0-AXS, R-CA0-AXX through
R-CA0-BAZ, R-CA0-BFE through R-CA0-BHY, R-CA0-BJS,
R-CA0-BKE, R-CA0-BKG-H, R-CA0-BKJ-K, R-CA0-BKP through
R-CA0-BKS, R-CA0-BKU-V, R-CA0-BLY through R-CA0-BMA,
R-CA0-BMC through R-CA0-BME, R-CA0-BNS, R-CA0-BOB through
R-CA0-BOJ, R-CA0-BPA through R-CA0-BRG, R-CA0-BBA through
R-CA1-BDA, R-CA1-BHZ through R-CA1-BUF, R-CA1-BJR,
R-CA1-BJT through R-CA1-BKE, R-CA1-BKD, R-CA1-BKF,
R-CA1-BKI, R-CA1-BKT, R-CA1-BLE, R-CA1-BLH through
R-CA1-BLN, R-CA1-BLS, R-CA1-BLU-V, R-CA1-BMN, and
R-CA1-BLE. The resulting pool represented 20% of the
final driver population. c) a pool of about 15,000 clones
from non-normalized libraries CS0s, CT0s, CU0s, CM0s, CX0s
and normalized libraries CS0, CT0, CU0, CM0, and CX0
corresponding to plates R-CS0s-CBD through R-CS0s-CBO,
R-CT0s-CAM through R-CT0s-CAS, R-CU0s-CBP through
R-CU0s-CCA, R-CM0s-CCB through R-CM0s-CCM, R-CX0s-CCN
through R-CX0s-CCX, R-CS0-BSD, R-CS0-BTD through R-CS0-BTV
R-CS0-BVM, R-CT0-BTW through R-CT0-BUP, R-CT0-BVN,
R-CU0-BUQ through R-CU0-BVL, R-CM0-BVY through R-CM0-BWP,
R-CX0-BXN through R-CX0-BXO, R-CX0-BWQ through R-CX0-BXM.
The resulting pool represented 5% of the final driver
population. d) a pool of about 5,000 clones (1,000 from
non-normalized eye library CV0 and 4,000 from normalized
eye library CV1) corresponding to plates R-CV0-BRH through
R-CV0-BRR, R-CV1-BRS through R-CV1-BSC, R-CV1-BSE through
R-CV1-BTC, and R-CV1-BVO through R-CV1-BVU. This pool
represented about 5% of the final driver population. e) A
pool of about 10,000 clones from subtracted library BS2,
BV0 and BVOP (7-9.5 kb cDNA library fraction from rat
whole embryo), and BX0 (0.5-7kb cDNA library fraction from
rat whole embryo) corresponding to plates R-BS2-BDB
through R-BS2-BFB, R-BV0-ANK through R-BV0-ANR, R-BVOP-AOI
through R-BVOP-AOX, and R-BX0-AOY through R-BX0-ASH. The
resulting pool represented 5% of the final driver
population. f) a pool of about 7,000 clones from the
seven non-normalized libraries that make up the tracer
including CY0, CZ0, DA0, DB0, DC0, DD0, and DE0
corresponding to plates R-CY0-BXP through R-CY0-BXZ,
R-CZ0-BYA through R-CZ0-BYI, R-DA0-BZB-C, R-DA0-BYJ
through R-DA0-BYP, R-DA0-BZD through R-DA0-BZH, R-DB0-BYQ
through R-DB0-BZA, R-DC0-BZI through R-DC0-BZQ, R-DC0-CAV
through R-DC0-CBA, R-DD0-BZR through R-DD0-CAI,
R-DD0-CBB-C, and R-DE0-CAB through R-DE0-CAL. The
resulting pool represented about 10% of the final driver

population. g) a pool of about 2,000 clones from the pool
of normalized libraries, CU0, that makes up the tracer.
The corresponding plates are R-CNO-BKW through R-CNO-BLD,
R-CNO-BLG, R-CNO-BLP through R-CNO-BLR, R-CNO-BLT,
R-CNO-BLW-X, R-CNO-BMB, and R-CNO-BMF through R-CNO-BML.
This pool represented 5% of the final driver population.
h) a pool of the 28 most abundant clones in the CNO pool
corresponding to the following addresses: bkx-a-09-0-UI,
bkx-b-09-0-UI, bkx-b-11-0-UI, bkx-b-10-0-UI, bkx-d-01-0-UI,
bkx-d-06-0-UI, bkx-g-08-0-UI, bkx-h-12-0-UI,
bkx-a-05-0-UI, bkz-a-06-0-UI, bkz-a-11-0-UI, bkz-c-06-0-UI,
bkz-c-09-0-UI, bkz-d-10-0-UI, bla-a-01-0-UI,
bla-a-02-0-UI, bla-f-04-0-UI, bla-g-07-0-UI, bla-g-12-0-UI,
blb-a-12-0-UI, blb-f-02-0-UI, blc-a-11-0-UI,
blc-e-95-0-UI, bid-1-08-0-UI, bid-f-02-0-UI, bid-g-04-0-UI,
blr-a-05-0-UI, blt-f-08-0-UI. This pool represented 5%
of the final driver population. i) One abundant CNO clone
(corresponding to the address bkz-a-11-0-UI) was digested
with Not I and Eco RI and the resulting insert was gel
purified. This purified insert was added directly to the
driver so that it represented 5% of the final driver
population.
TAG-LIB-UI-R-CNI
TAG-TISSUE-cervix
TAG-SEO-GACCA"

BASE COUNT 157 a 194 g 202 t 1 others
ORIGIN

Query Match 29.5%; Score 552.8; DB 13; Length 765;
Best Local Similarity 90.1%; Pred. No. 1.9e-57;
Matches 609; Conservative 0; Mismatches 52; Indels 15; Gaps 1;

136 TGAGTATATACACTTGTGATACACTCTGATGAGAGAGGGGTGAGAGATGATACCA 195
105 TGAATATATACACTTGTGATACACTCTGATGAGAGAGGGGTGAGAGATGATACCA 164
196 ACAAGGAACCCCTGCTCCGGGATGAAACGTCATTCATATAGATGATCTTCCGCCACCA 255
165 ACAAGGAACCCCTGCTCCGGGATGAAACGTCATTCATATAGATGATCTTCCGCCACCA 224
256 TCTACTTCATATCTTCTTCTGAGCATAGTGGCATGATGTTGGTATCTGTCATGG 315
225 TCTATTTATATCTTCTTCTGAGCATAGTGGCATGATGTTGGTATCTGTCATGG 284
316 GTTACCAAGAACCTTAAG 375
285 GTTACCAAGAACCTTAAG 344
376 ACCTCTCTTGTGATCATCACTCCCTCTTGGGAGTTGATGCCATGAGTACTGATCT 435
345 ACCTCTCTTGTGATCATCACTCCCTCTTGGGAGTTGATGCCATGAGTACTGATCT 404
436 TTGGGAATTTTGTGTAAGCTGTCCATATCATCTTACACTGTACACTCTACAGCAGC 495
405 TTGGGAATTTTGTGTAAGCTGTCCATATCATCTTACACTGTACACTCTTACAGCAGC 464
496 TTTCATCTCCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 555
465 TTTCATCTCCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 524
556 GTCAAGGCAAGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 615
525 GCCAGAGGCGGAG 584
616 CCCCTCTCTTCTGATCACTTCTGATCACTTCTGATCACTTCTGATCACTTCTGATCA 675
585 CCCCTCTCTTCTGATCACTTCTGATCACTTCTGATCACTTCTGATCACTTCTGATCA 637
676 AGGGGAGATGAGAGATCTGTACAGCCCTTTTACCCGAGATGAGCTGTGATGAGTGT 735
638 -----GGCAGGATCTGTGTACAGCCCTTTTACCCGAGATGAGCTGTGATGAGTGT 689
736 TTCAATTCCAGCAT 795

Db		690	TCCAGTTCACGACAATCATATCGGTGGGTCTCATTCCCTCGGGGCATGCTATCTCTCTGTT	749
Qy		796	ACTGCATATCATCTTC 811 	
Db		750	ACTGCATCATCATCTTC 765	
RESULT 14				
BGI45042				
LOCUS	BGI45042	582 bp	mRNA	linear EST 01-FEB-2001
DEFINITION	U75a01.y1 Soares_mouse_MNGB.bccl1 Mus musculus cDNA clone			
IMAGE:	3333409 5' similar to SW:CCR4_MOUSE P70658 C-X-C CHEMOKINE RECEPTOR type 4 ; mRNA sequence.			
KEYWORDS	BGI45042			
ACCESSION	BGI45042.1	GI:12648446		
VERSION	EST.			
ORGANISM	house mouse.			
SOURCE	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
TITLE	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)			
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapsb-f@mail.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MG1:1077573			
COMMENT	Seq primer: -40RP from Gibco High quality sequence stop: 503. Location/Qualifiers			
FEATURES				
source	1..582 /organism="Mus musculus" /db_xref="taxon:10090" /clone="IMAGE:3333409" /clone_lib="Soares_mouse_MNGB.bccl1" /lab_host="DH10B (phage-resistant)" /note="Organ: germinal B-cell; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I, Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTAACAATCTGAAGTGAGCGCGCGCGTGTCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested w/ht Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library is normalized; constructed by Bento Soares and M.Felima Bonaldo."			
COUNT	123 a	184 c	129 g	145 t 1 others
ORIGIN				
Query Match	29.4%	Score 551.6;	DB 12;	Length 582;
Best Local Similarity	98.1%;	Pred. No. 5.2e-57;		
Matches 568;	Conservative 0;	Mismatches 10;	Indels 1;	Gaps 1;
Qy	612	CCAGCCCCCCTCCGACATATCACTGACATCTTGGCGAGCGACGAGGGGACATC	671	
Db	1	CCAGCCCTCCCTCGACATATCACTGACATCTTGGCGAGCGACGAGGGGACATC	60	
Qy	672	AGTCAGGGGGATGACAGGTACATCTGTGACCCTTAAACCCGATVAGCTGTGGATGGT	731	
Db	61	AGTCAGGGGGATGACAGGTACATCTGTGACCGCCTTAAACCCGATVAGCTGTGGATGGT	120	
Qy	732	GTGTTTCAATTCCAGCATATATGTTGGGTTCTAATCTGCCGSCATGCTATCTCTCC	791	
Db	121	GTGTTTCAATTCCAGCATATATGTTGGGTTCTAATCTGCCGSCATGCTATCTCTCC	180	
Qy	792	TGTTACGTCATCATCTCTAACCTGTGACACATCCAAAGGGCCACCAAGCCGAAGGCC	851	
Db	181	TGTTACGTCATCATCTCTAACCTGTGACACATCCAAAGGGCCACCAAGCCGAAGGCC	240	

QY	852	CTCAAGACAGCATATCCATCCATCCATCTTCTTGGCTGCTGCTGCACATATTATG	911
Db	241	CTCAAGACAGCATATCCATCCATCTTCTTGGCTGCTGCTGCACATATTATG	300
QY	912	GGGATCAGCATCGACTCCCTTATCTCTTTGGGAGTCATCAAGCAAGATGTGACTTCGAG	971
Db	301	GGGATCAGCATCGACTCCCTTATCTCTTTGGGAGTCATCAAGCAAGATGTGACTTCGAG	360
QY	972	AGCATTTGTCACAAAGTGATGATCCATTCACAGAGGCCCTTGCTTTCACATGTTGCTG	1031
Db	361	AGCATTTGTCACAAAGTGATGATCCATTCACAGAGGCCCTTGCTTTCACATGTTGCTG	420
QY	1032	AAACCCATCTCTATGACCTTCTGCGGGGCGCAAGTTCAAAAGCTGCGCCACATGACATC	1091
Db	421	AAACCCATCTCTATGACCTTCTGCGGGGCGCAAGTTCAAAAGCTGCGCCACATGACATC	480
QY	1092	AACCTCATGACAGAGGCGCTCCAGGCTCCAGATCTCTTCCAAAGGAAAGCGGGTGACAC	1151
Db	481	AACCTCATGACAGAGGCGCTCCAGGCTCCAGATCTCTTCCAAAGGAAAGCGGGTGACAC	540
QY	1152	TCCTCCGCTCTCCAGGAGTCAAGATCTCCACAGTTTTCAC	1190
Db	541	TCCTCCGCTCTCCAGGAGTCAAGATCTCCACAGTTTTCAC	578
RESULT 15			
LOCUS	BT761664	827 bp	mRNA linear EST 25-SEP-2001
DEFINITION	603046395F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186878 5',		
ACCESSION	BT761664		
VERSION	BT761664.1	GI:15753242	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 827)		
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cs9abs-remail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	cDNA Library Preparation: Life Technologies, Inc.		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov		
	Plate: L14M11466 row: m column: 23		
	High quality sequence stop: 827.		
FEATURES	Location/Qualifiers		
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	/clone="IMAGE:5186878"		
	/clone_lib="NIH_MGC_116"		
	/lab_host="DH10B"		
	/note="Organ: pooled colon, kidney, stomach; Vector: PCWV-SPOrt6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."		
BASE COUNT	190 a 232 c 194 g 210 t	1	Others
ORIGIN			

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 15:03:23 ; Search time 235 Seconds
(without alignments)
12611.805 Million cell updates/sec

Title: US-09-367-052-1

Perfect score: 1877
Sequence: 1 ccatcctaatacactact.....aaaaaaaaaaaaaaaaa 1877

Scoring table: IDENTITY_NIC
Gapop 10.0 , Gapext 1.0

Number of hits satisfying chosen parameters: 2210862

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Published Applications-NA:

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	974.4	51.9	1737	9 US-09-104-063-3	Sequence 3, Appl1
2	952.8	50.8	1679	9 US-10-225-567A-75	Sequence 75, Appl1
3	944.8	50.3	1670	10 US-09-880-107-2143	Sequence 2143, Ap
4	808	43.0	1102	9 US-09-870-759-143	Sequence 143, App
5	576.4	30.7	1902	10 US-09-953-692-1	Sequence 1, Appl1
6	576.4	30.7	1902	10 US-09-953-692-1	Sequence 1, Appl1
7	303.2	16.2	421	9 US-09-796-692-2611	Sequence 2611, Ap
8	303.2	16.2	421	9 US-10-040-862-2611	Sequence 2611, Ap
9	287	15.3	487	9 US-09-796-692-8936	Sequence 8936, Ap
10	287	15.3	487	9 US-10-040-862-8936	Sequence 8936, Ap
11	198.4	10.6	1119	9 US-10-251-385-65	Sequence 65, Appl1
12	198.4	10.6	1679	9 US-09-104-063-5	Sequence 65, Appl1
13	198.4	10.6	2824	9 US-10-225-567A-59	Sequence 59, Appl1
14	196.8	10.5	1119	9 US-10-251-385-19	Sequence 19, Appl1
15	193.8	10.3	1107	9 US-10-251-385-19	Sequence 19, Appl1
16	193.8	10.3	1670	9 US-10-225-567A-73	Sequence 73, Appl1
17	193.8	10.3	1670	10 US-09-880-107-383	Sequence 383, Ap
18	193	10.3	1877	9 US-10-106-698-2125	Sequence 2125, Ap
19	192.2	10.2	1107	9 US-10-251-385-173	Sequence 173, App

20	188.8	10.1	1068	9 US-10-237-563-45	Sequence 45, Appl1
21	185	9.9	1068	9 US-10-237-563-47	Sequence 47, Appl1
22	182.8	9.7	1068	9 US-10-237-563-43	Sequence 43, Appl1
23	182.8	9.7	1068	9 US-10-237-563-44	Sequence 44, Appl1
24	182	9.7	1137	9 US-10-251-385-73	Sequence 73, Appl1
25	182	9.7	2139	9 US-10-225-567A-67	Sequence 67, Appl1
26	181.4	9.7	1068	9 US-10-237-563-48	Sequence 48, Appl1
27	181.4	9.7	1074	9 US-10-251-385-23	Sequence 23, Appl1
28	181.4	9.7	2462	9 US-10-225-567A-240	Sequence 240, App
29	181.4	9.7	2577	9 US-09-966-755-1	Sequence 1, Appl1
30	181.4	9.7	2577	10 US-09-903-377-1	Sequence 1, Appl1
31	181.4	9.7	2577	10 US-09-952-385-1	Sequence 1, Appl1
32	181.4	9.7	2577	12 US-10-000-759A-1	Sequence 1445, Ap
33	180.4	9.6	1318	10 US-09-917-800A-1445	Sequence 15, Appl1
34	179.8	9.6	2050	9 US-09-940-240-15	Sequence 42, Appl1
35	179.6	9.6	1068	9 US-10-237-563-42	Sequence 462, App
36	179.6	9.6	2456	9 US-10-225-567A-462	Sequence 203, App
37	178.8	9.5	1137	9 US-10-251-385-203	Sequence 175, App
38	178.2	9.5	1074	9 US-10-251-385-175	Sequence 41, Appl1
39	178	9.5	1068	9 US-10-237-563-41	Sequence 1, Appl1
40	178	9.5	1933	9 US-09-104-063-1	Sequence 46, Appl1
41	177.8	9.5	1068	9 US-10-237-563-46	Sequence 385, App
42	177.8	9.5	2856	9 US-10-225-567A-385	Sequence 38, Appl1
43	176.2	9.4	1068	9 US-10-237-563-38	Sequence 40, Appl1
44	173	9.2	1053	9 US-10-237-563-40	Sequence 627, App
45	171.8	9.2	2081	12 US-10-044-090-627	

ALIGNMENTS

RESULT 1
US-09-104-063-3
Sequence 3, Application US/09104063
Patent No. US20020168356A1
GENERAL INFORMATION:
APPLICANT: Lee, James
TITLE OF INVENTION: PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,063
FILING DATE: 24-June-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/701265
FILING DATE: 22-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/664228
FILING DATE: 06-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2C2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-104-063-3

Query Match 51.98; Score 974.4; DB 9; Length 1737;
Best Local Similarity 76.18; Pred. No. 4,7e-220;
Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

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350 GTACCGGCTGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 409
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780 GCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 839
890 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 949

840 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
950 CAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1009
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1250 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1309
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1850 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1877
1684 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1711

RESULT 2
US-10-225-567A-75
; Sequence 75, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences

APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 75
LENGTH: 1679
TYPE: DNA
ORGANISM: Homo sapiens
US-10-225-567A-75

Query Match 50.8%; Score 952.8; DB 9; Length 1679;

Best Local Similarity 80.2%; Pred. No. 5,9e-215; Mismatches 252; Indels 46; Gaps 6;

824 CTCGAAGGCGACAGAGGCGAGGCGCTCAAGACAGACATGATCTCATCTT 883
772 CTCGAAGGCGACAGAGGCGAGGCGCTCAAGACAGACATGATCTCATCTT 831
884 CTTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943
832 CTTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 891
944 AGTCATCAAGCAAGAGATGACTTCAGAGCATGCTGCAACAGTGTATCCATCA 1003
892 AATCATCAAGCAAGAGATGACTTCAGAGCATGCTGCAACAGTGTATCCATCA 951
1004 GGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1063
952 GGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1011
1064 GTTCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123
1012 ATTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1071
1124 CTTTCCAAAGCAAGAGATGACTTCAGAGCATGCTGCAACAGTGTATCCATCA 1183
1072 CTTTCCAAAGCAAGAGATGACTTCAGAGCATGCTGCAACAGTGTATCCATCA 1131
1184 TTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1243
1132 TTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1183
1244 GAACTTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1303
1184 ACTTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1243
1304 TTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1363
1244 TTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1297
1364 TTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1423
1298 GACTTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1353
1424 GTTCCAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1483
1354 GTTCCAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1405
1484 AACTGAACATTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543
1406 AACTGAACATTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1465
1544 GCTGCATA 1551
1466 TATGCATA 1473

824 CTCGAAGGCGACAGAGGCGAGGCGCTCAAGACAGACATGATCTCATCTT 883
772 CTCGAAGGCGACAGAGGCGAGGCGCTCAAGACAGACATGATCTCATCTT 831
884 CTTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943
832 CTTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 891
944 AGTCATCAAGCAAGAGATGACTTCAGAGCATGCTGCAACAGTGTATCCATCA 1003
892 AATCATCAAGCAAGAGATGACTTCAGAGCATGCTGCAACAGTGTATCCATCA 951
1004 GGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1063
952 GGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1011
1064 GTTCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123
1012 ATTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1071
1124 CTTTCCAAAGCAAGAGATGACTTCAGAGCATGCTGCAACAGTGTATCCATCA 1183
1072 CTTTCCAAAGCAAGAGATGACTTCAGAGCATGCTGCAACAGTGTATCCATCA 1131
1184 TTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1243
1132 TTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1183
1244 GAACTTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1303
1184 ACTTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1243
1304 TTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1363
1244 TTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1297
1364 TTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1423
1298 GACTTTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1353
1424 GTTCCAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1483
1354 GTTCCAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1405
1484 AACTGAACATTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543
1406 AACTGAACATTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1465
1544 GCTGCATA 1551
1466 TATGCATA 1473

RESULT 3
US-09-880-107-2143.
Sequence 2143, Application us/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2143

SEQ ID NO 143
 LENGTH: 1102
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (44)..(1102)
 OTHER INFORMATION:
 US-09-870-759-143

Query Match 43.0%; Score 808; DB 9; Length 1102;
 Best Local Similarity 85.9%; Pred. No. 7.7e-181;
 Matches 914; Conservative 0; Mismatches 135; Indels 15; Gaps 1;

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OY 136 TGAGTATATACACTCTGTCTGATCTGCTGGAAGTGGGCTGGAGACTGTGACTCCA 195
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Db 54 TGAGTATATACACTCTGTCTGATCTGCTGGAAGTGGGCTGGAGACTGTGACTCCA 113

OY 196 ACAAGGAACCCCTGCTCCGGGATGAAACGCTCCATTTCATAGATCTTCTGCCCCACCA 255
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Db 114 TGAAGAACCCCTGTTCCGTGAAGAAATGTAATTTCAATTAATCTTCTGCCCCACCA 173

OY 256 TCTACTTATCATCTTCTTGAAGCTGATGCTGCAATGATGTTGGTATCTGCTGATG 315
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Db 174 TCTACTTATCATCTTCTTGAAGCTGATGCTGCAATGATGTTGGTATCTGCTGATG 233

OY 316 GTTACAGAGAAGCTAAGGAGCATGACGAGCAATGACCGGCTGACCTGAGTGGCTG 375
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 234 GTTACAGAGAAGCTAAGGAGCATGACGAGCAATGACCGGCTGACCTGAGTGGCTG 293

OY 376 ACCCTCTCTTTGTCACACACTCCCTTCTGGGAGTTGATGCCATGCTGCTGCTGCT 435
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Db 294 ACCCTCTCTTTGTCACACACTCCCTTCTGGGAGTTGATGCCATGCTGCTGCTGCTGCT 353

OY 436 TTGGGAATTTTGTGTAGGCTGTCCATATCATCTACACTGTCAACCTCTACAGACGC 495
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 354 TTGGGAATTTTGTGTAGGCTGTCCATATCATCTACACTGTCAACCTCTACAGACGC 413

OY 496 TTCTGATCTGCTGCTGATCAGCTGAGCGGCTGACCTGCTGCTGCTGCTGCTGCTG 555
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Db 414 TTCTGATCTGCTGCTGATCAGCTGAGCGGCTGACCTGCTGCTGCTGCTGCTGCTGCTG 473

OY 556 GTCAAGGCAAGAACTGTGCTGAAAGGAGCTGATGCTGCTGCTGCTGCTGCTGCTG 615
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 474 GTCAAGGCAAGAACTGTGCTGAAAGGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 533

OY 616 CCCTCTCTGCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 534 CCCTCTCTGCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 578

OY 676 AGGGGATGAGAGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 735
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 579 AGGGGATGAGAGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 638

OY 736 TTCAATTCAGATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 795
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 639 TTCAATTCAGATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 698

OY 796 ACTGATCATCTCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 855
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 699 ACTGATCATCTCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 758

OY 856 AGAGCAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 915
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 759 AGAGCAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 818

OY 916 TGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 975
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 819 TGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 878

OY 976 TTGTGACAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1035
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 879 TTGTGACAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 938
  
```

RESULT 5
 US-09-953-692-1
 ; Sequence 1, Application US/09953692
 ; Patent No. US20020107195A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shalley, Gupta K.
 ; TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by
 ; FILE REFERENCE: P50676C1
 ; CURRENT APPLICATION NUMBER: US/09/953,692
 ; PRIOR APPLICATION DATE: 2001-09-17
 ; PRIOR APPLICATION NUMBER: 09/358,624
 ; PRIOR FILING DATE: 1999-07-21
 ; PRIOR APPLICATION NUMBER: 60/093,596
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1902
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (158)(223)(225)(226)(335)(466)(520)(530)(645)(763)(825)(1120)
 ; LOCATION: (1183)
 ; US-09-953-692-1

Query Match 30.7%; Score 576.4; DB 10; Length 1902;
 Best Local Similarity 70.8%; Pred. No. 6.4e-126;
 Matches 1212; Conservative 26; Mismatches 243; Indels 231; Gaps 27;

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OY 1036 CCATCTCTATGCTCTTCTGCGGGCCAAAGTTCAAAAGCTGCCGAGTGCATCACT 1095
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Db 939 CCATCTCTATGCTCTTCTTCTGAGGCAATTTAAACCTCTGCGCAGCAGCAGTCACT 998

OY 1096 CCATGAGCAGAGGCTCCAGCCTCAAGATCTTTCGAAAGAAAGCGGGGTGACACTGT 1155
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 999 CTGTGACAGAGAGGCTCCAGGCTCAAGATCTCTCCAAAGAAAGGAGGTGACATTCAT 1058

OY 1156 CCGTCTCCAGGAGTCCAGATCTCTCAGTTTTCATCTCCAGCTAA 1199
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Db 1059 CTGTTCACACTGAGTCTGATCTTCAAGTTTCACTCCAGCTAA 1102

OY 312 ATGGGTTACAGAGAAGCTAAG-----GAGCATGAGGAGCAAGTACCGGCTG 359
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 308 ATGGGTTACAGAGAAGCTAAGAGAGNGVMGKRRSCATGACGACAAGTACAGGCTG 367

OY 360 CACCTGTAGTGGCTGACCTCTCTG-----TCACTACACTCCCTTCTGGG 408
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 368 CACCTGTAGTGGCTGACCTCTCTG-----TCACTACACTCCCTTCTGGG 427
  
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OY		409	CAGTTGATGCCACGGCGTGCAGCTGGATCACTTT-----GGGAATTGTGTGGTAGG	456
Dd		428	CAGTTTGATGCCGTGGCACAACACTGGTACTTTTVMADVAVNMVGGGAACCTCTAATGCAAGG	487
OY		457	CTGTCCATATCATGTACACACTGTCAACCCSTTA-----CAGCAGCCGTTCATAC	503
Dd		488	CAGTCCATGTCACTATACACACTCAACCCGTGAKGNKAVHVVTVNVCAGACAGTGTCTCATC	547
OY		504	CTGGCCTTTCATACGCTTGGACC GGTA CCGCTCGCC-----ATTGTCCACGCCACAC	554
Dd		548	CTGGCCTTTCATACGCTTGGACC GGTA CCGCTCGCCSVASVDRYATCTCCACGCCACAC	607
OY		555	AGTCAAAAGGCCCAAGAAAACCTGTGGCTGAAAAGGCA-----GTCTATGTGGGCG	603
Dd		608	AGTCAAGAGGCCCAAGAAAACCTGTGGCTGAAAAGHATNSRRKAKGTGGCTATGTGGCG	667
OY		604	TCTGGATCCGACCCCTCTCTCTGACTATACTGACTTATCTTTGGSCGACGCTCACGCCAGG	663
Dd		668	TCTGGATCCGACCCCTCTCTCTGACTATACTGACTTATCTTCCGANVVUVGVWAT-----DCTCATCTTTGG	722
OY		664	GGAACATTCAGTACAGGGGGATGACAGAGTAATCTGTGAC-----GCCTTTACCCC	712
Dd		723	CCAACGTCAGAGAGGACAGATGACAGATATCTGTGACACANVSADDRXCDCGCTCTACCC	782
OY		713	CGATAGCCCTGTGATAGTGCGTGCTTCAATTCACACATAT-----AATGGTGGGCT	763
Dd		783	CAATGACTTGTGGGTGGTGTGTGTTCCAGTTTCCACACATCRXNDMVUVAHHHTTGGGCT	842
OY		764	CATCTCGCCCGGACATCTGCATCTCTCTCTGTACTGATC-----ATCATCTCTAA	814
Dd		843	TATCTCGCTGTGTATGTGCATCTCTCTCTGTATGTGATIMGVSYCTATCATCTCCAA	902
OY		815	CGTGTCACTTCCAAAGGGCCACCAAGAAGCCAAAGGCC-----TCAAGACGAC	862
Dd		903	CGTGTCACTTCCAAAGGGCCACCAAGAAGCCAAAGGCCSKSHKHKRKAICAGACACAC	962
OY		863	AGTATCTCTCATCTAGCTTTCTTGGCTGTGGCTGC-----CATATATCTGGGG	914
Dd		963	AGTATCTCTCATCTAGCTTTCTTGGCTGTGGCTGTGGCTGTAAVCACTAACATTTGGG	1022
OY		915	ATCAGCATCGACCTCTTCATCTCTTTGGAGATCAATCAA-----GCAAGATGTGACTT	967
Dd		1023	ATCAGCATCGACCTCTTCATCTCTCTCTGAAATCATCAAYUSDBSKCAAGSGTGTGACTT	1082
OY		968	CGAAGCATTTGSCAACAAGTGATCTCCATCAG-----AGGCCCTGCGCTTCT	1017
Dd		1083	TGAACAACACTGTGCACAAGTGATGATTCATCAGCGCNTVHKMSTGAGCCCTACTCTTCT	1142
OY		1018	TCCACCTGTGGCTTAACCCCCATCTCTATGCTTTC-----CTGGGGGCGAAGTTCAA	1069
Dd		1143	TCCACCTGTGTCTAAMCCCCATCTCTATGTCTTCAHCNCNVACTTGGAGGCCAAATTTAA	1202
OY		1070	AAGCTCTCTCCGAGATGCATCAACTC-----CATGAGCAGAGGCTCCAGCC	1116
Dd		1203	AAGCTCTCTCCGAGATGCATCAACTCCTGTGTAGAGAKTSMHATSVSCAGAGGGTCCAGCC	1262
OY		1117	TCAAGATCTTTTCCAAAGGAAGCGGGGTGACACT-----CTTCCGTCTCC	1163
Dd		1263	TCAAGATCTCTCCAAAGGAAGGAGGTGACATPTRESSSKRKRGHNACTGTCTCC	1322
OY		1164	ACGGAGTCAGAACTCTCAGTTTTTCACTCCAGCTA--ACCTTTATGCAAGACTTTATATA	1221
Dd		1323	ACTGAGTGTGAGTCTTCAAGTTTTTCACTCCAGCTAACSSVSSTSSHHSHTAGTGTAAA	1382
OY		1222	ATATATATATATATATGATTAAGAACTTTTTAT--GTACACATTTTCCAGATATAGA	1279
Dd		1383	AGACTTTTTTTATATACGATTAATATACTTTTTTTAAgTATACATTTTTCAGATATAAAA	1442
OY		1280	GACTGACAGCTCTGTACAGTTTTTTTTTTTTTTTTTAAATGCACTGTGGAGATTAATCTTC	1339
Dd		1443	GACTGACCAATATGTACAGTTTTTTATTTCTGTGTGGATTTTTGT-----CTTGTGTCTT	1496
OY		1340	CTCTAGTTTTTGTAGAGCTTGCACCTAAATATATATATGTTTTTGTGTGTCTCATG	1399

Db	1497	CTTAGTATTTTGTGACAGTTTAATTGACTATTATTAA-----TAAATTTTTTTTGTTTCATA	1555
QY	1400	TGAATGAGCGTCTTAGCCAGCAGCTGTGGCCAA GTTCTTAGAGCTGTTTATCTGTGTGTA	1455
Db	1553	TTGATGTGTCTAGCGAGCACCTGTGGCCAA GTTCTTAGTGTGCTGTATGTCGTGCTA	1612
QY	1460	GCACTGTAGCACTGTAGAGCAAGAACAATCCAGCAATGTGTGGTAAATTGCATATA	1519
Db	1613	GGACTGTAGAA-----AAGGGAACTGAAACATTCCAGACGCTGTAGTAATGATACGTTAA	1664
QY	1520	AGCTAGCCGTATCCTCAGCTGTGCTGCATA	1551
Db	1665	AGCTAGAAATCATCCCCAGCTGTTTATGCATA	1696
 RESULT 6 US-09-953-717-1			
Sequence 1, Application US/09953717			
Patent No. US20020107196A1			
GENERAL INFORMATION:			
APPLICANT: Shalley, Gupta K.			
TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by			
TITLE OF INVENTION: Administering Stromal Cell Derived Factor-1(
FILE REFERENCE: P50676D1			
CURRENT FILING DATE: 2001-09-17			
PRIOR APPLICATION NUMBER: 09/358,624			
PRIOR FILING DATE: 1999-07-21			
PRIOR APPLICATION NUMBER: 60/093,596			
PRIOR FILING DATE: 1998-07-21			
NUMBER OF SEQ ID NOS: 6			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 1			
LENGTH: 1902			
TYPE: DNA			
ORGANISM: Human			
FEATURE:			
NAME/KEY: unsure			
LOCATION: (158)(223)(225)(226)(335)(466)(520)(530)(645)(763)(825)(1120)			
LOCATION: (1183)			
US-09-953-717-1			
 Query Match 30.7%; Score 576.4; DB 10; Length 1902; Best Local Similarity 70.8%; Pred. No. 6.4e-126; Matches 1212; Conservative 26; Mismatches 243; Indels 231; Gaps 27;			
QY	44	GCAGGTGAGGTAGCAGTACCCTCTGTAGGCGTTGGTGCCTCCGTACCAACACCGCTG	103
Db	12	GCAGGAGGAGGTAGCAAAAGTACGCCGCGAGGCGCTGAGTGTCCATAGCCACCGCATGTG	71
QY	104	TAGAGCGAG-TGTTGCCATGGAACCGCATGTCAGTATGATATATACACTTCTGATACTACT	162
Db	72	GAGAACCCGCGGTATACCACTGAGAGGGATCM----GAGTATATACACTTCAGATATACATA	127
QY	163	CTGAAGAAGTGGGCTGTGAGACTA-----TGACTCCAACAAGAACCTG	208
Db	128	CCGAGGAATGTGCTCAGGGAGTASYSNDVYTMGSGDYTGACTGCATGAAAGAACCTG	187
QY	209	CTTCCGGGATTAANAACGTCCTTTTCATAG-----ATCTCTGCCACACATCT	258
Db	188	TTTTCCTGTAAMAATAATGCTAATTTCCAATADSMKCRNANNAATCTTCTGCCACACATCT	247
QY	259	ACTTCATCATTTCTTGACTGGCATATG-----CGCAATGATTTGGTATCCTGGTC	311
Db	248	ACTCATCATCTTTCTTAAGCTGGCATGTGTGTYSTGVGCAATTCGATTTGGTATCTCTGGTC	307
QY	312	ATGGGTTACCAAGAAGACTAAG-----GAGCATGAGCGAGCAAGATACCGGCTG	359
Db	308	ATGGGTTACCAAGAAGAACTAGAAAGNGVMGYKKRSCATGAGCGAGCAAGATACAGGCTG	367
QY	360	CACCTGTACGTGGCTGACCTCTCTCTTGG-----TCATCACACTCCCCTTCTTGGG	408


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Db      61 GGATCCCTGCCCCCTCCTGCTGACTATTTCCCGACTTCATCTTGGCAAGC----- 108
Oy      667 ACATAGTCAGGGGGATGACAGGTACATCTGTGACCGCTTACCCGATAGAGCTGTGGA 726
Db      109 ---TCAGGAGGACATACAGATATATCTGTGACCGCTTACCCGATAGCTGTGG 165
Oy      727 TGTGTTGTTTCATTTCCAGCATATATATGTTGGTCTCTATCTGCGCCGCAATCGTCATCC 786
Db      166 TGGTGTGTCTCCAGTTTACGACATCATGTTGGCTTATCTGCTGTGTAATGTCATCC 225
Oy      787 TCTCTGTCTACTGATCATCTATCTTAAGCTGTACACTCCAGGGCCACCAAGAGCCGA 846
Db      226 TGTCTGTATTTATCTATCTTCACTCCAGCTGCACACTCCAGGGCCACCAAGAGCCGA 285
Oy      847 AGGCCCTCAAGACAGCATCTCTCATCTGACTTTTGGAGTCAATCAAGCAAGATGTGACT 906
Db      286 AGGCCCTCAAGACAGCATCTCTCATCTGACTTTTGGAGTCAATCAAGCAAGATGTGACT 345
Oy      907 ATGTGGGATGACATCTCTCTTTCATCTTTTGGAGTCAATCAAGCAAGATGTGACT 966
Db      346 ACATGGGATGACATCTCTCTTTCATCTTTTGGAGTCAATCAAGCAAGATGTGACT 405
Oy      967 TCGAGAGCATTTGTGCA 982
Db      406 TTGAGAACACTGTGTGCA 421
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RESULT 8

US-10-040-862-2611

; Sequence 2611, Application US/10040862
; Publication No. US20030078396A1

GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

; FILE REFERENCE: 014058-013520US

; CURRENT APPLICATION NUMBER: US/10/040,862

; CURRENT FILING DATE: 2001-11-06

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 60/222,903

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: US 60/223,416

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: US 60/223,378

; PRIOR FILING DATE: 2000-08-07

; PRIOR APPLICATION NUMBER: US 09/796,692

; PRIOR FILING DATE: 2001-03-01

; NUMBER OF SEQ ID NOS: 10467

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2611

; LENGTH: 421

; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-040-862-2611

Query Match

Best Local Similarity 83.3%; Score 303.2; DB 9; Length 421;
Matches 363; Conservative 0; Mismatches 58; Indels 15; Gaps 1;

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Oy      547 CCACCAACAGTCACCAAGGCAAGAAAGCTGCGGTGAAAGGAGAGTATATGAGCGCT 606
Db      1 CCACCAACAGTCACAGGCAAGGCAAGAGCTGTTGGCTGAAAGAGTATATGAGCGCT 60
Oy      607 GGATCCAGCCCTCCTCTGACTATACCTGACTTATCTTATCTTGGAGCTGAGCCAGG 666
Db      61 GGATCCCTGCTCCTCTGCTGACTATCCCGACTTATCTTGGCAAGC----- 108
Oy      667 ACATAGTCAGGGGATGACAGGTACATCTGTGACCGGCTTACCAGATAGCGTGTGGA 726
Db      109 ---TCAGTGGGACAGATACAGATATATCTGTGACCGGCTTACCAGATAGCTGTG 165
Oy      727 TGTGTTGTTTCATTTCCAGCATATATATGTTGGTCTCTATCTGCGCGCATCTGTCATCC 786
Db      166 TGGTGTGTCTCCAGTTTACGACATCATGTTGGCTTATCTGCTGTGTAATGTCATCC 225
Oy      226 TGTCTGTATTTATCTATCTTCACTCCAGCTGCACACTCCAGGGCCACCAAGAGCGCA 285
Oy      286 AGGCCCTCAAGACAGCATCTCTCATCTGACTTTTGGAGTCAATCAAGCAAGATGTGACT 906
Db      346 ACATGGGATGACATCTCTCTTTCATCTTTTGGAGTCAATCAAGCAAGATGTGACT 405
Oy      907 ATGTGGGATGACATCTCTCTTTCATCTTTTGGAGTCAATCAAGCAAGATGTGACT 966
Db      346 ACATGGGATGACATCTCTCTTTCATCTTTTGGAGTCAATCAAGCAAGATGTGACT 405
Oy      967 TCGAGAGCATTTGTGCA 982
Db      406 TTGAGAACACTGTGTGCA 421
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RESULT 9

US-09-796-692-8936/c

; Sequence 8936, Application US/09796692

; Publication No. US20020198362A1

GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER

; FILE REFERENCE: 2077_001200

; CURRENT APPLICATION NUMBER: US/09/796,692

; CURRENT FILING DATE: 2001-03-01

; PRIOR APPLICATION NUMBER: 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: 60/222,903

; PRIOR FILING DATE: 2000-08-03

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; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 8936
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-8936

Query Match      15.3%; Score 287; DB 9; Length 487;
Best Local Similarity 77.6%; Pred. No. 7e-58;
Matches 392; Conservative 0; Mismatches 95; Indels 18; Gaps 3;

QY 923 CGACTCTTCATCCTTTTGGAGTCAATCAAGCAGATGACTTGAGACATTTGCA 982
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DB 487 CGACTCTTCATCCTTCCTGGAATCAATCAAGCAGGCTGTGAGTTGAGACACTGTGA 428
    983 CAAGTGATCTCCATCAGACAGAGCCCTCGCTTCCACTGTGCTGACCCCATCCT 1042
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 427 CAAGTGATCTTCATCAGCAGAGCCCTACCTTTCTTCCACTGTGCTGACCCCATCCT 368
    1043 CTATGCTTCTCTCGGGGCCAAGTTCAAAAGCTCTGCCAGCATGCACTCACTCATGAG 1102
    ||||| ||||| ||| ||| ||| ||||| ||||| ||||| ||||| |||||
DB 367 CTATGCTTCTCTGGAGCCAAATTTAAACCTCTGCCAGCAGCAGCTCAGCTCTGTGAG 308
    QY 1103 CAGAGGCTCCAGCCTCAAAATCTTTCCAAAGAGAAAGCGGGGTGACACTCTTCGCTTC 1162
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 307 CAGAGGCTCCAGCCTCAAAATCTTTCCAAAGAGAAAGCGGGGTGACACTCTTCGCTTC 248
    1163 CAGGAGTCAGAACTCTCCAGTTTTCACCCAGCTACACCTTATGCAAGACTATATATA 1222
    ||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
DB 247 CACTGAGTCTGAGCTTTCAGATTTCACCTCACTCA-----CACAGATGTAAAGA 196
    QY 1223 TATATATATATATATGATAAAGAACTTTTATGTTACACATTTTCCAGATATAGAGAC 1282
    ||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
DB 195 CTTTCTTTTATAGATAAATACTTTTATGTTACACATTTTCCAGATATAGAGAC 136
    1283 TGACCACTCTTGACAGTTTCTTTTATGTTACACTGTGGAGTTTATGTTCC 1342
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 135 TGACCAATATTTGACAGTTTATGCTTGTGATTTTGT-----CTTGCTTTCTT 82
    1343 TAGTTTGTGAGGTTGACTTAATTTATATATAATTTGTTTGTGTTTCATGTGA 1402
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 81 TAGTTTGTGAGTTTATGACTTATTTATA-----TAAATTTTGTGTTTCATTTG 26
    1403 ATGAGCGTCTAGCAGACCTGTGG 1427
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 25 ATGTGTGTCTAGCAGACCTGTGG 1
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
US-10-040-862-8936/c
; Sequence 8936, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-01352005
; CURRENT APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
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; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 8936
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-8936

Query Match      15.3%; Score 287; DB 9; Length 487;
Best Local Similarity 77.6%; Pred. No. 7e-58;
Matches 392; Conservative 0; Mismatches 95; Indels 18; Gaps 3;

QY 923 CGACTCTTCATCCTTTTGGAGTCAATCAAGCAGATGACTTGAGACATTTGCA 982
    ||||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
DB 487 CGACTCTTCATCCTTCCTGGAATCAATCAAGCAGGCTGTGAGTTGAGACACTGTGA 428
    983 CAAGTGATCTCCATCAGACAGAGCCCTCGCTTCCACTGTGCTGACCCCATCCT 1042
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 427 CAAGTGATCTTCATCAGCAGAGCCCTACCTTTCTTCCACTGTGCTGACCCCATCCT 368
    1043 CTATGCTTCTCTCGGGGCCAAGTTCAAAAGCTCTGCCAGCATGCACTCACTCATGAG 1102
    ||||| ||||| ||| ||| ||| ||||| ||||| ||||| ||||| |||||
DB 367 CTATGCTTCTCTGGAGCCAAATTTAAACCTCTGCCAGCAGCAGCTCAGCTCTGTGAG 308
    QY 1103 CAGAGGCTCCAGCCTCAAAATCTTTCCAAAGAGAAAGCGGGGTGACACTCTTCGCTTC 1162
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 307 CAGAGGCTCCAGCCTCAAAATCTTTCCAAAGAGAAAGCGGGGTGACACTCTTCGCTTC 248
    1163 CAGGAGTCAGAACTCTCCAGTTTTCACCTCAACCTTATGCAAGACTATATATA 1222
    ||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
DB 247 CACTGAGTCTGAGCTTTCAGATTTCACCTCACTCA-----CACAGATGTAAAGA 196
    QY 1223 TATATATATATATATGATAAAGAACTTTTATGTTACACATTTTCCAGATATAGAGAC 1282
    ||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
DB 195 CTTTCTTTTATAGATAAATACTTTTATGTTACACATTTTCCAGATATAGAGAC 136
    1283 TGACCACTCTTGACAGTTTCTTTTATGTTACACTGTGGAGTTTATGTTCC 1342
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 135 TGACCAATATTTGACAGTTTATGCTTGTGATTTTGT-----CTTGCTTTCTT 82
    1343 TAGTTTGTGAGGTTGACTTAATTTATATATAATTTGTTTGTGTTTCATGTGA 1402
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 81 TAGTTTGTGAGTTTATGACTTATTTATA-----TAAATTTTGTGTTTCATTTG 26
    1403 ATGAGCGTCTAGCAGACCTGTGG 1427
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 25 ATGTGTGTCTAGCAGACCTGTGG 1
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-10-251-385-65
; Sequence 65, Application US/10251385
```

Publication No. US20030105292A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030105292A1- Endogenous, Constitutively Activated Human G
TITLE OF INVENTION: Protein-coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 65
LENGTH: 1119
TYPE: DNA
ORGANISM: Homo sapiens
US-10-251-385-65

Query Match 10.6%; Score 198.4; DB 9; Length 1119;
Best Local Similarity 53.8%; Pred. No. 1.1e-36;
Matches 456; Conservative 0; Mismatches 386; Indels 6; Gaps 2;

231 TTCAATAGATCTTCTGCGCCACCATCTTATCATGCTTCTTGAAGTGGAGTGGG 290
145 TTCAAGGCGCTGTCTGCGCCGCGGCTTACAGCTTATCTTCTGCGGCGATCGG 204
291 AATGATGATGATCTTCTGCTGATGATGATGATGATGATGATGATGATGATG 350
205 AACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 264
351 TACGGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 410
265 TTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 324
411 GTTATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 470
325 GCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 384
471 TACATGCTCAACCTTCAACGACGCTTCTCATCTGCTGCTGCTGCTGCTGCTG 530
385 CACAAGTCAACCTTCAACGACGCTTCTCATCTGCTGCTGCTGCTGCTGCTGCT 444
531 CTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 590
445 CTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 504
591 GTTATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 650
505 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 564
651 GACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 710
565 AAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 624
711 C---CGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 767
625 CAAGCAGAAAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 684
768 CTGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 827
685 CTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 744
828 AA---GGCGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 884
745 CACGCGCGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 804
885 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 944
805 TTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864

945 GTCATCAAGCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1004
865 GCCGTGAGCAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 924
1005 GCCGTGAGCAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1064
925 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 984

1065 TTCAAAAG 1072
985 TTCCGCGAG 992

RESULT 12
US-09-104-063-5
Sequence 5; Application US/09104063
Patent No. US20020168356A1
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Wood, William I.
TITLE OF INVENTION: PD4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,063
FILING DATE: 24-June-1998
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/701265
FILING DATE: 22-AUG-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/664228
FILING DATE: 06-JUN-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706p2C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-104-063-5

Query Match 10.6%; Score 198.4; DB 9; Length 1679;
Best Local Similarity 53.8%; Pred. No. 1.4e-36;
Matches 456; Conservative 0; Mismatches 386; Indels 6; Gaps 2;

231 TTCAATAGATCTTCTGCGCCACCATCTTATCATGCTTCTTGAAGTGGAGTGGG 290
513 TTCAAGGCGCTGTCTGCGCCGCGGCTTACAGCTTATCTTCTGCGGCGATCGG 572

[illegible]

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;
; NUMBER OF SEQ ID NOS: 2292
;
; SOFTWARE: Patentinl version 3.1.1
;
; SEQ ID NO 59
;
; LENGTH: 2824
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
US-10-225-567A-59

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Query Match	10.6%	Score 198.4	DB 9	Length 2824
Best Local Similarity	53.8%	Pred. No. 2e-36		
Matches 456; Conservative	0	Mismatches 386	Indels 6	Gaps 2

OY	231	TTCAATAGACATCTTCCTCCCAACCACTTACTTATCTATCATCTCTTACAGGCAATACGCCG	290
OY	229	TTTCAAGCGCGCTTGTGTGTCGCCGTGGCTTACAGCCATCTTCTCTGTGGCGTATCGCG	288
OY	291	AATGATTTGTATCTCTGTATCGGTTACAGAGAAGCTAAGGAGCATGCGACAAG	350
Db	289	AACGTCCTGCTGTGTATCTCTGGAGGGGACCGGGAGACACGAGTTCCACAGAGACC	348
OY	351	TACGGGCTGCACTGTGAGTGGCTGACCTCCCTTGTATCATCACACTCCCTCTGGGGA	410
Db	349	TTCTGTTCCACCTGGCCCTGGCGGACCTCTCGTGTCTTATCTTGGCTTTCGGG	408
OY	411	GTTGATGCCATGGCTGATCTGTACTTTTGGAAATTTTGTGAAGGCTGTCATATCATC	470
Db	409	GCCGAGGCGCTGTGGGCTGGGCTCTGGGAGACTTCCTGTGCAAAACTGTATGTGCGCTG	468
OY	471	TACACTGTCAACCTTACAGACGCTTCTCATCTGCGCTTATATAGCTTGACGGGTAC	530
Db	469	CACAAAGTCACTTCTACTGTAGGACGACGCTGCTCTGCGCTGTGATGGCCCTGGACGGCTAC	528
OY	531	CTGGCATTTGTACAGGCACCAACAGTAAAGGCCAAGAACTCTGGCTGAAAAAGCA	590
Db	529	CTGGCATTTGTACAGCGCTCATCGCTCATACGCCACACGGCGGCTCTCTCATTCACATC	588
OY	591	GCTATGTGGGCGTGTGATCCAGCCCTCTCTGACTATACGTGACTTCAATCTTTGCC	650
Db	589	ACCTGTGGAGCACTCTGGCTGTGGGCTTCTCTTGGCTTCCAGAGATCTCTTTCGCGC	648
OY	651	GACGTCACCCAGGGGAGACATGATCAGGGGGATGACAGTACATCTGTATACCGGCTTTCAC	710
Db	649	AAAGTCACCCAGGCCATCACACACACTCCCTGCCACGTTGACACTTCTCCCAAGAGATC	708
OY	711	C---CCGATAGCCTGTGATGGTGTGTTTCATTTCCAGCATATATAGTGGGTCTCATATC	767
Db	709	CAAGCAGAAACGATGCGCTGTGCTACCTCCGATTTCTCTACATGTGGCGGATTTCTGTG	768
OY	768	CTGCCCGGCAATCTCTCTCTCTCTGTATCTGATCATCATCATCTCTTAAGCTGTACACTTC	827
Db	769	CTGCCCATGCTGTGATGATGGCTGTGCTACGTGGGGGTAGTGCACAGTGTGGCCAGGCGC	828
OY	828	AA---GGGCGACCAAGAGCGACCCCTCAAGAGAGAGTATCTCATCTACTACTTTTC	884
Db	829	CAGCGGCGCCCTCAGCGGAGAGAGCAAGCAATCAGGTGGGCAATCTGTGTACAGCATCTTC	888
OY	885	TTTGCTCTCTGCTGCTGCATATATATGTGGAGATCAGACTGCACTCTCTATCTTTGGGA	944
Db	889	TTCTCTCTCTGTGTACCTTACCATCATCTCTCTTCTTGAGAACCTTGCGAGCGTGAAG	948
OY	945	GTCATATCAGCAAGAGATGTGACTGTGAGAGCATTTGTGCACAAAGTGAATCTCATCACAGG	1004
Db	949	GCGGTGACATATCTGTCAAGCTGATGGCTCTCTCCCGTGGCCATCATCAGATGTGTAGG	1006
OY	1005	GCCCTGCGCTTCTTCCACTGTGGCTGAAACCCCATCTATGCTCTCTCTGGGGCCAG	1066
Db	1009	TTCTGCGGCGCTGGGCCACTGTGCTCAACCCCATGCTCTACACTTTTGGCGGCGTGAAG	1066
OY	1065	TTCAAAAG 1072	
Db	1069	TTCCGAG 1076	

RESULT 14
US-10-251-385-199
; Sequence 199, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 199
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-251-385-199

Query Match 10.5%; Score 196.8; DB 9; Length 1119;
Best Local Similarity 53.7%; Pred. No. 2.6e-36;
Matches 455; Conservative 0; Mismatches 387; Indels 6; Gaps 2;

QY 231 TTCAATAGATCTCTCTGCCACCATCTATCTATCTCTCTGAGTGGC 290
DB 145 TTCAAGCGCGTGTCTGCGCCGCTGAGCTACAGCTCTCTCTGAGTGGC 204
QY 291 AATGATGATGATCTCTGCGCTGAGTGGTACAGAAAGAGTAAAGAGTAAAG 350
DB 205 AACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 264
QY 351 TACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 410
DB 265 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 324
QY 411 GTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470
DB 325 GCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 384
QY 471 TACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 530
DB 385 CACAAGTCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444
QY 531 CTGCGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 590
DB 445 CTGCGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 504
QY 591 GTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 650
DB 505 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 564
QY 651 GACGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 710
DB 565 AAGAGTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 624
QY 711 C---CGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 767
DB 625 CAGAGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 684
QY 768 CTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 827
DB 685 CTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 744
QY 828 AAGGCGCAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 884
DB 745 CAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 804
QY 885 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 944

DB 805 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864
QY 945 GTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1004
DB 865 GCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 924
QY 1005 GCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1064
DB 925 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 984
QY 1065 TTCAAAAG 1072
DB 985 TTCCCGAG 992

RESULT 15
US-10-251-385-19
; Sequence 19, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human
; TITLE OF INVENTION: Protein-coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-251-385-19

Query Match 10.3%; Score 193.8; DB 9; Length 1107;
Best Local Similarity 52.2%; Pred. No. 1.3e-35;
Matches 463; Conservative 0; Mismatches 412; Indels 12; Gaps 1;

QY 181 GAGCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 101 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 160
QY 241 TCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 161 CCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 220
QY 301 TGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 221 TGGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 280
QY 361 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 281 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 340
QY 421 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 341 CCGTCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 400
QY 481 ACCTTACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 401 ACCTTACAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 460
QY 541 TCCAGGCGCAGAGAGTCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 461 TTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 520
QY 601 GCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 13:44:23 ; Search time 305 Seconds
(without alignments)
13859.019 Million cell updates/sec

Title: US-09-367-052-1

Perfect score: 1877

Sequence: 1 ccatcctaatacgaactcact.....aaaaaaaaaaaaaaaaaaaaa 1877

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

A number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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- 7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
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- 14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1875.4	99.9	1877	19	AAV46370
2	1758	93.7	1758	20	AAZ27611
3	974.4	51.9	1737	16	AAO80521
4	974.4	51.9	1737	16	AAO90007
5	969.6	51.7	1737	13	AAO29506
6	952.8	50.8	1679	22	AAI65467
7	952.8	50.8	1679	22	AAI12801
8	951.8	50.7	1664	21	AAA61656
9	951.8	50.7	1664	21	AAZ40014

10	944.8	50.3	1670	24	ABK83803	Human CDNA differe
11	944.8	50.3	1670	24	ABN95645	Gene #2143 used to
12	939.8	50.1	1944	20	AAV15882	CDNA encoding G-pr
13	936.8	49.9	1588	20	AAZ27610	Human CXCR4 coding
14	934	49.8	5161	21	AAE20896	Human CCR-4 CC che
15	934	49.8	5161	21	AAA34774	Human adenosine re
16	934	49.8	5161	24	AAH99951	CXCR4 gene. Homo
17	834.6	44.5	1317	19	AAV18357	Human RM3 seven tr
18	834.6	44.5	1317	21	AAA9726	Human 7TM receptor
19	834.6	44.5	1317	24	ABK54255	Human 7 Transmembr
20	833	44.4	1317	15	AAQ66179	Seven transmembran
21	809.6	43.1	1059	21	AAZ38553	Human CX-C-chemok
22	809.6	43.1	1059	24	AAH99952	CXCR4 encoding seq
23	804.8	42.9	1059	23	ABT97982	Non-endogenous hum
24	739.6	39.4	1119	24	AAK98241	Human cysteine-X-C
25	410.4	21.9	606	24	ABA92962	Human CDNA clone D
26	282	15.0	440	21	AAQ01917	Human secreted pro
27	203.2	10.8	611	20	AAV15883	CDNA encoding a pa
28	198.4	10.6	1119	21	AAA30626	Human G protein-co
29	198.4	10.6	1679	13	AAQ37107	New platelet facto
30	198.4	10.6	1679	16	AAQ99009	Chemokine superfam
31	198.4	10.6	1679	16	AAQ80522	Human lymphocyte p
32	198.4	10.6	2818	20	AAK87710	Human Burkitt's ly
33	198.4	10.6	3620	22	ABA09117	Human Burkitt lymph
34	196.8	10.5	1119	21	AAA30727	DNA encoding human
35	195.8	10.4	2072	24	AAV17156	Mouse lymphoid spe
36	195.8	10.4	2084	24	ABK54274	Mouse 7 transmembr
37	195.8	10.4	2085	21	AAK91745	7TM receptor DNA s
38	193.8	10.3	1107	21	AAA30593	Human G protein-co
39	193.8	10.3	1670	19	AAV26557	Human IP-10/Mig re
40	193.8	10.3	1670	24	ABN97338	Gene #3836 used to
41	193	10.3	1877	22	AAH35033	Human colon cancer
42	192.2	10.2	1107	21	AAA30714	DNA encoding human
43	192.2	10.2	1159	20	AAZ32713	Human chemokine re
44	192.2	10.2	1876	18	AAV72800	Human G-protein ch
45	189	10.1	4017	23	AAK83768	DNA encoding novel

ALIGNMENTS

RESULT 1	AAV46370	standard: cDNA to mRNA: 1877 BP.
ID	AAV46370	
AC	AAV46370;	
DT	20-NOV-1998	(first entry)
XX		
DE	Nucleic acid encoding a murine CXC chemokine receptor.	
XX		
KW	Mouse: CXC chemokine receptor; pre-B cell line DW34;	
KW	CXC chemokine pre-B cell stimulatory factor PBSP/SDF-1;	
KW	HIV infection; screening; inhibitor; AIDS; ds.	
XX		
OS	Mus sp.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	120..1199
XX		/*tag= a
XX		
PN	MO9835035-A1.	
PD	13-AUG-1998.	
XX		
PF	07-FEB-1997;	97WO-JP00299.
XX		
PR	07-FEB-1997;	97WO-JP00299.
XX		
PA	(SHIO) SHIONOGI & CO LTD.	
XX		
PI	Iizasa H, Kishimoto T, Nagasawa T, Nakajima T, Tachibana K;	
PI	Yoshida N, Yoshie O;	

XX WPI: 1998-447232/38.
DR P-PSDB: AAW64778.
XX
PT Mouse CXK chemokine receptor binding to PBSF/SDF-1 pre-B cell
stimulatory factor - is useful for screening of potential HIV
infection and AIDS inhibitors
XX
PS Claim 3: Pages 39-42; 76pp; Japanese.
XX
CC The present sequence encodes a murine CXK chemokine receptor which
binds to the mouse CXK chemokine pre-B cell stimulatory factor
PBSF/SDF-1. The nucleic acid is isolated from mouse pre-B cell
line DM34. The receptor and cells expressing it can be used in the
study and mapping of the mechanism of HIV infection and in screening
of potential inhibitors of HIV infection and the development of AIDS.
XX
SQ Sequence 1877 BP; 469 A; 451 C; 406 G; 551 T; 0 other;

Query Match 99.9%; Score 1875.4; DB 19; Length 1877;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCTTAATACGACTCACTATAGGCTGAGCGGCCGCCGGGAGGTGACAGTACGAG 60
DB 1 CCATCTTAATACGACTCACTATAGGCTGAGCGGCCGCCGGGAGGTGACAGTACGAG 60
QY 61 TGACCCCTGAGGCGTTTGGTCTCCGGTAACACCGAGGCTGTAGAGCGAGTTGGCA 120
DB 61 TGACCCCTGAGGCGTTTGGTCTCCGGTAACACCGAGGCTGTAGAGCGAGTTGGCA 120
QY 121 TGGAACGATCAGTGTAGTATATACACTTGTATACACTCTGTAAGAAGTGGGGTCTG 180
DB 121 TGGAACGATCAGTGTAGTATATACACTTGTATACACTCTGTAAGAAGTGGGGTCTG 180
QY 181 GAGACTATACCTCAACAGAGAACCTGCTCCGGATGAAAAAGCTTTCATATAGA 240
DB 181 GAGACTATACCTCAACAGAGAACCTGCTCCGGATGAAAAAGCTTTCATATAGA 240
QY 241 TCTTCTGGCCACACTCTACTCATCTTCTTGTGATGATGAGCATAGCGCATAGATTTG 300
DB 241 TCTTCTGGCCACACTCTACTCATCTTCTTGTGATGATGAGCATAGCGCATAGATTTG 300
QY 301 TGATCTGTGATCGGTGTACCAAGAGAGCTAAGAGCATGAGCGACAAGTACCGGCTGC 360
DB 301 TGATCTGTGATCGGTGTACCAAGAGAGCTAAGAGCATGAGCGACAAGTACCGGCTGC 360
QY 361 ACCTGTCAGTGGGTGACCTCTTGTGATCACAACCTCCCTTGGGAGTTGATGCCA 420
DB 361 ACCTGTCAGTGGGTGACCTCTTGTGATCACAACCTCCCTTGGGAGTTGATGCCA 420
QY 421 TGGCTGACTGTACTTTGGAAATTTTGTAAAGCTGTCATATCATCTACACGTGA 480
DB 421 TGGCTGACTGTACTTTGGAAATTTTGTAAAGCTGTCATATCATCTACACGTGA 480
QY 481 ACCTGTACAGACGCTTCTATCTGCGCTTATCAGCTGAGCCGATCTCGCATTTG 540
DB 481 ACCTGTACAGACGCTTCTATCTGCGCTTATCAGCTGAGCCGATCTCGCATTTG 540
QY 541 TCCAGCGCCCAACAGTCAAAAGGCCAAGAACTGCTGATAAAAGAGTCTATAGTG 600
DB 541 TCCAGCGCCCAACAGTCAAAAGGCCAAGAACTGCTGATAAAAGAGTCTATAGTG 600
QY 601 GGGTGTGATCCAGGCTCTCTGACTATACCTGACTTCACTTTGCGGAGCTGAGCC 660
DB 601 GGGTGTGATCCAGGCTCTCTCTGACTATACCTGACTTCACTTTGCGGAGCTGAGCC 660
QY 661 AGGGGACATCAGTCAAGGGGATGACAGGTACATCTGTGACCGCTTTATCCCGATAGCC 720
DB 661 AGGGGACATCAGTCAAGGGGATGACAGGTACATCTGTGACCGCTTTATCCCGATAGCC 720
QY 721 TGTGATGTTGTTTCAATTCCAGCATATATGTTGGTCTCATCTGCCCGGATTCG 780
DB 721 TGTGATGTTGTTTCAATTCCAGCATATATGTTGGTCTCATCTGCCCGGATTCG 780

DB 721 TGTGATGTTGTTTCAATTCCAGCATATATGTTGGTCTCATCTGCCCGGATTCG 780
QY 781 TCATCTCTCCGTGTACGATCATCATCTCACTGACAGTGCACAGCCACGCA 840
DB 781 TCATCTCTCCGTGTACGATCATCATCTCACTGACAGTGCACAGCCACGCA 840
QY 841 AGCGAAGGCGCTCAAGAGAGACAGTCACTATCTTGTGCTGCTGCTGCTG 900
DB 841 AGCGAAGGCGCTCAAGAGAGACAGTCACTATCTTGTGCTGCTGCTGCTGCTG 900
QY 901 CATATATGTGGGATCAGATCAGATCTCTTATCTTTTGGAGTATCAAGAGAT 960
DB 901 CATATATGTGGGATCAGATCAGATCTCTTATCTTTTGGAGTATCAAGAGAT 960
QY 961 GGTACTTCCAGAGCATTTGTGCAAGTGTGATCTCATACAGAGGCCCTTCTTCC 1020
DB 961 GGTACTTCCAGAGCATTTGTGCAAGTGTGATCTCATACAGAGGCCCTTCTTCC 1020
QY 1021 ACTGTTGCTGAACCCATCTCTATGCTTCTGCGGCGCAAGTTCAAAAGCTTGC 1080
DB 1021 ACTGTTGCTGAACCCATCTCTATGCTTCTGCGGCGCAAGTTCAAAAGCTTGC 1080
QY 1081 AGCATGACTCACTCATGATGACAGAGCTCCAGCTCAAGATCTTTTCAAGAAAGC 1140
DB 1081 AGCATGACTCACTCATGATGACAGAGCTCCAGCTCAAGATCTTTTCAAGAAAGC 1140
QY 1141 GGGGTGACACTCTTCCGTCCTCAGAGATCAAGATCTTCCATCTCAGCTTAC 1200
DB 1141 GGGGTGACACTCTTCCGTCCTCAGAGATCAAGATCTTCCATCTCAGCTTAC 1200
QY 1201 CCTATGCAAGACTTATATATATATATATATATATATATATATATATATATAT 1260
DB 1201 CCTATGCAAGACTTATATATATATATATATATATATATATATATATATATAT 1260
QY 1261 ACATTTTCCAGATATAGAGACTGACAGCTCTTGTACAGTTTATTTTATATGA 1320
DB 1261 ACATTTTCCAGATATAGAGACTGACAGCTCTTGTACAGTTTATTTTATATGA 1320
QY 1321 CTGTTGGAGTTATGTTTCTAGTTTGTGAGAGTTGACTTATATATATATAT 1380
DB 1321 CTGTTGGAGTTATGTTTCTAGTTTGTGAGAGTTGACTTATATATATATATAT 1380
QY 1381 GTTTTTTGTGTTTCAATGATGATGAGCTGTAGAGAGCTGTGGCAAGTCTTAT 1440
DB 1381 GTTTTTTGTGTTTCAATGATGATGAGCTGTAGAGAGCTGTGGCAAGTCTTAT 1440
QY 1441 AGCTGTTATCTGTGTGATGAGCTGTAGAGAGCTGTAGAGAGAGAGAGAGAG 1500
DB 1441 AGCTGTTATCTGTGTGATGAGCTGTAGAGAGCTGTAGAGAGAGAGAGAGAG 1500
QY 1501 TGTGTGTAAATGATTAAGAGCTAGCCGATCTCAGCTGTGCTGATATATCTTCA 1560
DB 1501 TGTGTGTAAATGATTAAGAGCTAGCCGATCTCAGCTGTGCTGATATATCTTCA 1560
QY 1561 TTTCCAGAGAGACCCACCCACCCACCCACCCACCCACCCATCTTAAATGTTGGTAT 1620
DB 1561 TTTCCAGAGAGACCCACCCACCCACCCACCCACCCACCCATCTTAAATGTTGGTAT 1620
QY 1621 GCTGTGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1680
DB 1621 GCTGTGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1680
QY 1681 AGATGACATTAAGCAAGAGCTAAGATGATGATGATGATGATGATGATGATGAT 1740
DB 1681 AGATGACATTAAGCAAGAGCTAAGATGATGATGATGATGATGATGATGATGAT 1740
QY 1741 GTTTGTTTTCAGTTTCAAGAGTATGATGATGATGATGATGATGATGATGATGAT 1800
DB 1741 GTTTGTTTTCAGTTTCAAGAGTATGATGATGATGATGATGATGATGATGATGAT 1800
QY 1801 TATTACATTTGTTTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
DB 1801 TATTACATTTGTTTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1860

OY 1861 AAAAAAAAAAAAAAAAAA 1877
 |||
 Db 1861 AAAAAAAAAAAAAAAAAA 1877

RESULT 2
 AA227611
 ID AA227611 standard; DNA; 1758 BP.

AA227611:

16-DEC-1999 (first entry)

Mouse CXCR4 coding sequence.

CXCR4; mouse; neovascularisation; inhibitor; solid cancer; therapy;
 tissue repairing agent; vascularisation; ss.

Mus sp.

WO948528-A1.

30-SEP-1999.

23-MAR-1999; 99WO-JP01448.

24-MAR-1998; 98JP-0095448.

(CHUS) CHUGAI SEIYAKU KK.

(KISH/) KISHIMOTO T.

Kishimoto T, Nagasawa T, Tachibana K;

WPI: 1999-591042/50.

P-PDB: AAT99994.

Vascularisation inhibitors

Disclosure; Page 50-51; 63pp; Japanese.

This sequence encodes the mouse CXCR4 protein. The invention relates to
 remedies inhibiting neovascularisation, remedies for solid cancer,
 remedies for diseases pathologically caused by neovascularisation and
 tissue repairing agents containing as the active ingredient a substance
 capable of potentiating CXCR4. Based on a finding that vascularisation is
 inhibited in a CXCR4 knockout mouse, it becomes possible to prepare
 remedies inhibiting vascularisation which contain as the active
 ingredient a substance capable of potentiating CXCR4, remedies for solid
 cancer, remedies for diseases pathologically caused by neovascularisation
 and tissue repairing agents containing as the active ingredient a
 substance capable of potentiating CXCR4. It is also possible to establish
 methods for treatment with the use of these remedies.

Sequence 1758 BP; 447 A; 414 C; 369 G; 528 T; 0 other;

Query Match 93.7%; Score 1758; DB 20; Length 1758;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1758; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 120 ATGAACCGATAGTGTGATATACCTCTGATACTCTGAGAAAGTGGGTCT 179

Db 1 ATGAACCGATAGTGTGATATACCTCTGATACTCTGAGAAAGTGGGTCT 60

OY 180 GGAGACTATGACTCCAAAGGAACCTGCTTCGGGATGAAACGTCATTCAATAGG 239

Db 61 GGAGACTATGACTCCAAAGGAACCTGCTTCGGGATGAAACGTCATTCAATAGG 120

OY 240 ATCTTCTGCGCCCATCTACTCATCTCTTACAGCGCATTCGGCATGATG 299

Db 121 ATCTTCTGCGCCCATCTACTCATCTCTTACAGCGCATTCGGCATGATG 180

OY 300 GTGATCTGTGATGGTTACGAGAAAGCTAAGAGCATGACGAGCAAGTACGGCTG 359

Db 181 GTGATCTGTGATGGTTACGAGAAAGCTAAGAGCATGACGAGCAAGTACGGCTG 240

OY 360 CACCTGTGATGGTGTGACTCTCTTTGTCATACACTCCCTCTTGGGCACTGTATGCC 419

Db 241 CACCTGTGATGGTGTGACTCTCTTTGTCATACACTCCCTCTTGGGCACTGTATGCC 300

OY 420 ATGGCTGATGGTGTGAAATTTTGTGTAAAGCTGTGCATATCATCTACACTGTC 479

Db 301 ATGGCTGATGGTGTGAAATTTTGTGTAAAGCTGTGCATATCATCTACACTGTC 360

OY 480 AACCTGTACAGAGCGTTCTCATCTGCGCTTCATAGCGTGGACGCTACCTCGCATT 539

Db 361 AACCTGTACAGAGCGTTCTCATCTGCGCTTCATAGCGTGGACGCTACCTCGCATT 420

OY 540 GTCCACGCCACCAACAGTAAAGGCCAAGAAACCTGCTGTGAAAGGCACTATGTG 599

Db 421 GTCCACGCCACCAACAGTAAAGGCCAAGAAACCTGCTGTGAAAGGCACTATGTG 480

OY 600 GGGCTGTGATGCCACGCCCTCCTGACTATACCTGACTTCATCTTTCGCGACGTCGAC 659

Db 481 GGGCTGTGATGCCACGCCCTCCTGACTATACCTGACTTCATCTTTCGCGACGTCGAC 540

OY 660 CAGGGGACATCAGTACAGGGGGATGACAGGTACATCTGTGACCGCTTTACCCGATACG 719

Db 541 CAGGGGACATCAGTACAGGGGGATGACAGGTACATCTGTGACCGCTTTACCCGATACG 600

OY 720 CTGTGATGCTGTGTTTCAATTCACGATATATGTGGTCTCATCTCGCCGCGATC 779

Db 601 CTGTGATGCTGTGTTTCAATTCACGATATATGTGGTCTCATCTCGCCGCGATC 660

OY 780 GTCATCTCTCCGTTACTGATCATCATCTCTAAGCTGTACACATCCAAAGGCGACGAC 839

Db 661 GTCATCTCTCCGTTACTGATCATCATCTCTAAGCTGTACACATCCAAAGGCGACGAC 720

OY 840 AAGCGCAAGGCCCTCAAGACGACATCTCATCTCTGCTTCTTCTGCTGCTGCTG 899

Db 721 AAGCGCAAGGCCCTCAAGACGACATCTCATCTCTGCTTCTTCTGCTGCTGCTG 780

OY 900 CCATATATATGTGGGATTCAGCATCTGACTCTTTCATCTTTCGAGATCATCAAGCAAGA 959

Db 781 CCATATATATGTGGGATTCAGCATCTGACTCTTTCATCTTTCGAGATCATCAAGCAAGA 840

OY 960 TGGACTTGGAGGCTTGGACAGTGTGATCTCATCAAGAGGCGCTGCTGCTGCTG 1019

Db 841 TGGACTTGGAGGCTTGGACAGTGTGATCTCATCAAGAGGCGCTGCTGCTGCTG 900

OY 1020 CACTGTGCTGTAACCCCATCTCTTATGCTTCTGCGGGGCAAGTTCAAAAGCTCTGCC 1079

Db 901 CACTGTGCTGTAACCCCATCTCTTATGCTTCTGCGGGGCAAGTTCAAAAGCTCTGCC 960

OY 1080 CAGCATGCACTCACTTCATGACAGAGGCTCCAGCTCAAGATCTCTTCCAAAGANG 1139

Db 961 CAGCATGCACTCACTTCATGACAGAGGCTCCAGCTCAAGATCTCTTCCAAAGANG 1020

OY 1140 CGGGGTGGACACTCTCGCTCCAGGAGTCAGATCCCAAGTTTCTACCTCCACTTAA 1199

Db 1021 CGGGGTGGACACTCTCGCTCCAGGAGTCAGATCCCAAGTTTCTACCTCCACTTAA 1080

OY 1200 CCTTATGCAAGACTTAT 1259

Db 1081 CCTTATGCAAGACTTAT 1140

OY 1141 CACATTTTCCAGATATATAGAGACTGACAGCTTGTGACAGTTTCTTCTTCTTCTT 1200

Db 1320 ACTGTGGAGTATATGCTCTAGTTTGTGAGGTTTGTCTTATATATATATATATAT 1379

OY 1201 ACTGTGGAGTATATGCTCTAGTTTGTGAGGTTTGTCTTATATATATATATATAT 1260

Db 1380 TGTCTTCTGCTTCTCATGTGAATGAGCTGACAGACTGCGCAAGTCTCTAG 1439

Dd		1261	TGTTTTTTTGGTTTTCATGTGAATGAGCGCTCTGACGAGACCCTGTGGCCAACTTCTTAG	1320
Oy		1440	TAGCTGTTTATCTGTGTGTAGACTGTAGAAGCTGTAGAGGAAGAACTGAACATTCCAGA	1499
Dd		1321	TAGCTGTTTATCTGTGTGTAGACTGTGAACTGTAGAGGAAGAACTGAACATTCCAGA	1380
Oy		1500	ATGTGTGTATAATTGAATAAAGCTAGCCGTATCCTCAGCTGTGTGCATTAATCTCTTC	1559
Dd		1381	ATGTGTGTATAATTGAATAAAGCTAGCCGTATCCTCAGCTGTGTGCATTAATCTCTTC	1440
Oy		1560	ATTCGAGAGACACCCCACCCCCACCCCCACCCCCCACTTTTAATTGTTGGTTA	1619
Dd		1441	ATTCGAGAGACACCCCACCCCCACCCCCACCCCCCACTTTTAATTGTTGGTTA	1500
Oy		1620	TGCTGTGTGATGTTTGTGTGTTTTTTTTTGTTGTGTGTGTTTTTTTTTCTGTAA	1679
Dd		1501	TGCTGTGTGATGTTTGTGTGTTTTTTTTTGTTGTGTGTGTTTTTTTTTCTGTAA	1560
Oy		1680	AAGATGGACATTAACAACCAAGCCGTGAATGSGTGTGAATGCTGGGGTTTTTTTCTT	1739
Oy		1561	AAGATGGACATTAACAACCAAGCCGTGAATGSGTGTGAATGCTGGGGTTTTTTTCTT	1620
Oy		1740	TGTTTGTGTTTTTTCAGTTTCAAGATGATGATTCCTCACCAATGTACAGTCTT	1799
Dd		1621	TGTTTGTGTTTTTTCAGTTTCAAGATGATGATTCCTCACCAATGTACAGTCTT	1680
Oy		1800	GTAATTACATTTGTAATAAAGCTCATGATGAATACTTAAAAAATTTAAAAAATTTAAA	1859
Dd		1681	GTAATTACATTTGTAATAAAGCTCATGATGAATACTTAAAAAATTTAAAAAATTTAAA	1740
Oy		1860	AAAAAAAAAAAAAAAAAAAAA 1877	
Dd		1741	AAAAAAAAAAAAAAAAAAAAA 1758	
 RESULT 3 AAQ80521 ID AAQ80521 standard; cDNA: 1737 BP.				
xx		AAQ80521:		
ac				
xx		18-JUL-1995 (first entry)		
dt				
xx				
de		Human monocyte PF4AR cDNA.		
xx				
kw		Interleukin-8 receptor; IL-8 receptor; PF4AR;		
kx		platelet factor superfamily receptor; monocyte; chemotactic;		
ky		inflammation; inflammatory disease; arthritis; emphysema; cystic;		
ky		fibrosis; colitis; bronchitis; meningitis; therapeutic; ss.		
os		Homo sapiens.		
xx				
fh		Key	Location/Qualifiers	
ft		CDS	91..1149	
et			/*tag= a	
xx				
pn		W09428931-A.		
pd		22-DEC-1994.		
xx				
pe		07-JUN-1994; 94WO-US06380.		
pr		11-JUN-1993; 93US-0076093.		
xx				
pa		(GENH) GENENTECH INC.		
xx				
pi		Chuncharapai A, Hebert C, Kim KJ, Lee J;		
xx				
dr		WPI; 1995-036114/05.		
dr		P-PSDB; AAR68812.		
pt		Treatment of inflammatory disorders - by administering an antibody capable of binding a platelet factor 4 superfamily		

Query Match	Best Local Similarity	Score	DB	Length
Matches 1391; Conservative	76.1%;	974.4;	16;	1737;
	0;	1.9e-174;		
		Mismatches 301;	Indels 136;	Gaps 10
Sequence 1737 BP; 454 A; 411 C; 373 G; 499 T; 0 other:				
50	GCAGTACCAAGTACACCTCTGTGAGGGCGTTGGTGTCCCGTACACCAACGCGTGTAGAC	109		
20	GGCGGGCCCAAGATGACCGCGGAGGGCCCTGAGTGTCCATGACCAACCGATGTGGGAAC	79		
110	GAGTGTGGCCATGGAACCGATCAGTGTGATATACATCTTGTATTAACCTACTGGAAGA	169		
80	CAGCGGTTTACCATGGA-----GGGATCAGTATATACACTTAGATTAACACCGAGAGA	134		
170	AGTGGGGTCTGGAGACTATGATCTCCACAAGGAACCGTCTTCGGGATGAAGAACGTCGA	229		
135	AATGGGCTCAGGGGACTATGATCATCTCATGAAAGAACCTGTTTCCGTAAGAAATGCTAA	194		
230	TTTCAATAGGATCTTCTGTCGCCACCATCTACTCTCATCTCTTGTAGCTGCGATAGTCGG	289		
195	TTTCAATATAATCTTCTGTCGCCACCATCTACTCTCATCTCTTGTAGCTGCGATAGTCGG	254		
290	CAATGATTTGGATCTGTCGTCATGGGTATCCAGAGAAGAAAGTAAAGAGCATGACGACAA	349		
255	CAATGATTTGGATCTGTCGTCATGGGTATCCAGAGAAGAAAGTAAAGAGCATGACGACAA	314		
350	GTACCGGCTGCACCTGTGATGTGCTGTCCTCTTGTGTATACACACTTCCCTTGTGGC	409		
315	GTACAGGCTGCACCTGTGATGTGCTGTCCTCTTGTGTATACACACTTCCCTTGTGGC	374		
410	AGTGTATGCCATCGCTGATCGTACTTTGGGAAATTTTGTGTAGGCTGTGCTCATATCAT	469		
375	AGTGTATGCCATCGCTGATCGTACTTTGGGAAATTTTGTGTAGGCTGTGCTCATATCAT	434		
470	CTACACTGTCAACTCTCTACAGAGCGTCTCTCATCTGTGGCTTCATACAGCGCTGACCGGTA	529		
435	CTACACTGTCAACTCTCTACAGAGCGTCTCTCATCTGTGGCTTCATACAGCGCTGACCGGTA	494		
530	CTCGGCCATTGTCAAGCGCCACCAACAGTCAAAAGGCGCAAGAAACTGTGGCTGAAGAGGC	589		
495	CTCGGCCATTGTCAAGCGCCACCAACAGTCAAAAGGCGCAAGAAACTGTGGCTGAAGAGGC	554		
550	AGTGTATGTGGCGCTGTGGATCCAGCGCTCTCTGACTATACCTGACTTATCTTTGCG	649		
555	GGCTATATTTGGCGCTGTGGATCCAGCGCTCTCTGACTATACCTGACTTATCTTTGCG	614		
650	CGAGCTCAGCCAGGGGGAGATCAGTCAAGGGGATGACAGGTATCATCTGTGACCGGCTTAA	709		
615	CAAGC-----TCAGTGAAGGACAGATACAGATATATCTGTGACCGGCTTAA	659		
710	CCCGCATAGCGTGTGGATGTGTGTTTCAATTTCCAGCATATAAATGGTGTGCTCATCTCT	769		
660	CCCGCATAGCTTGTGGATGTGTGTTTCAATTTCCAGCATATAAATGGTGTGCTCATCTCT	719		
770	GGCGGGCATGCTCATCTCTCTGTTTACTGACATCATCTCTAAGTGTCACTCCAA	829		
720	GGCTGTATTTGTCACTCTGCTCTGTTTGTGCTTTCATCTTCCAGCGTGTCACTCCAA	779		
830	GGGCGACCAAGGCGCAAGGCGCTCAACAGCAAGCACTCATCTCTGCTGCTTCTTCCG	889		
780	GGGCGACCAAGGCGCAAGGCGCTCAACAGCAAGCACTCATCTCTGCTGCTTCTTCCG	839		

QY	890	CTGCTGCTCCCAATATATATGTGGGAATCAGATCTGATCTTATCCTTTGGGAGATC	949
Db	840	CTGTGGCTGCTTACTACATTTGGGATCAGATCAGATCTTATCTCTGGAATCAT	899
QY	950	CAAGCAAGATGTGACTTTCGAGAGCAATTTGTCACAAATGATCTTCATCAGAGGCCCT	1009
Db	900	CAAGCAAGGGTGTGAGTTTGTAACACATGTGTCACAAATGATTTCCATCCGAGGCCCT	959
QY	1010	CGCTTCTTCACGTGTGCTGTAACCCCATCTCTATAGCTTCTCTGGGGCCAAATTCGA	1069
Db	960	AGCTTTCTTCACGTGTGTGTGAACCCCATCTCTATAGCTTCTCTGGAGCCAAATTTAA	1019
QY	1070	AAGCTTGGCCAGCATCCTCAACTCAATCAGACAGAGGCTCCAGCCTCAAGATCTCTTC	1129
Db	1020	AACCTGCGCCAGAGCACTCAACTCTGTGAGACAGAGGGTCCAGCCTCAAGATCTCTTC	1079
QY	1130	CAAAAGAAAGCGGGGTGGACACTCTTCCTCCAGAGACTCAAAATCTCCAGTTTCA	1189
Db	1080	CAAAAGGAAGCGGGGTGGACATTCATCTGTTTCCACATGACTGAGAGCTTCAAGTTTCA	1139
QY	1190	CTCCAGCTAACCCCTTATGCAAGACCTATATATATATATATATATATATATATATAT	1249
Db	1140	CTCCAGCTAA-----CAAGATGTAAAGACTTTTCTTTTATACATTAATTAATCTTTT	1191
QY	1250	TTTTATGTTACACATTTTCCAGATATTAAGAGACTGACACACTCTGTATACATTTT	1309
Db	1192	TTTTAATGTACACATTTTTCAGATATTAAGAGACTGACACATATATGTACAGTTT	1251
QY	1310	TTTTTAATTCAGCTTGGAGGTTTATGTCTCTAGTTTGTGGAGGTTTGACTTAATTT	1369
Db	1252	TTGTGTGATTTTGT-----CTTGGTCTTCTTATGTTTGTGAATTTTAATTTGACTTA	1305
QY	1370	ATATAAATATTTGTTTTTTTGTTCATCTGATGATGAGCTGCTGAGGAGGACCTGGGCC	1429
Db	1306	TTTATA-----TAATTTTTTTTGTTCATCTGATGATGAGCTGCTGAGGAGGACCTGGGCC	1361
QY	1430	AAGTCTTACAGCTTTTATCTGTGTGTAGAGACTGATGAACTGTAGAGGAAGAACTGA	1489
Db	1362	AAGTCTTACAGCTTTTATCTGTGTGTGTAGAGACTGATGAA-----AAGGAACTGA	1413
QY	1490	ACATTCAGAAATGTGTGTAATTTGAATTAAGCTAGCCGATGATCTGATCTGTGCTGCA	1549
Db	1414	ACATTCAGAGCGTGTATGTAATTTGATGATGATGATGATGATGATGATGATGATGATGAT	1473
QY	1550	TAACTCTTCATTCGAGAGACACCCACCCACCCACCCACCCACCCACCCATTTTAAT	1609
Db	1474	TATATATCTCTCCA-----	1488
QY	1610	TGTTTGGTTATGCTGTCTGATGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1669
Db	1489	-----TTCGCGGGAAGCTTTTCTCTGTTTCTTAAGACGTGAT	1525
QY	1670	TTTTCTGTAAAGATGCGACTTAATAAACCAAGCTGAATGTGTGTAAGATCTGTGGGT	1729
Db	1526	TTTGT	1581
QY	1730	TTTTTTTGT	1789
Db	1582	-----TTTTTTCAGTTTTCAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1623
QY	1790	GTACAGCTGTGTATATCATTTGTAATTAAGCTGAATGATTAACCTTAATAAAAAA	1849
Db	1624	GTACAGCTGTGTATATAGTTGTGTATATTAAGGTACATGTTAACCTTAATAAAAAA	1683
QY	1850	AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1877	
Db	1684	AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1711	

Query Match	Best Local Similarity	51.9%; Score 974.4; DB 16; Length 1737;
Matches 1391; Conservative	0; Mismatches 301; Indels 136; Gaps 10	
XX AAQ99007;		
DT 26-MAR-1996 (first entry)		
XX Chemokine superfamily receptor coding sequence.		
DE Interleukin; IL-8; inflammation; psoriasis; dermatitis;		
XX rheumatoid arthritis; inflammatory bowel disease;		
KW chronic lung inflammation; treatment; antibody;		
KW affinity purification; detection; ss.		
XX Homo sapiens.		
OS		
XX		
PN US5440021-A.		
XX		
PD 08-AUG-1995.		
XX		
PF 29-MAR-1991; 91US-0677211.		
XX		
PR 25-FEB-1994; 94US-0202056.		
PR 29-MAR-1991; 91US-0677211.		
XX		
PA (CHUN/) CHUNTHARAPAI A.		
PA (HEBE/) HEBERT C.		
PA (KIMK/) KIM K J.		
PA (LEEJ/) LEE J.		
XX		
PI Chuntharapai A, Hebert C, Kim KJ, Lee J;		
DR WPI; 1995-283151/37.		
DR P-PSDB; AAR80757.		
XX		
PT New antibodies against interleukin 8 type B receptor - used to treat		
PT or prevent inflammation, also for detecting receptor expression and		
PT purification.		
XX		
PS Example 2; Columns 47-50; 62pp; English.		
XX		
CC Antibodies directed against the interleukin-8 receptor B can be used		
CC to treat or prevent inflammation e.g. psoriasis, dermatitis,		
CC rheumatoid arthritis and particularly inflammatory bowel disease and		
CC chronic lung inflammation. When immobilised, these antibodies may		
CC be used to detect interleukin-8 receptor B expression in cells and		
CC tissues and for affinity purification of interleukin-8 receptor B		
CC from cells. This sequence is an additional chemokine superfamily		
CC receptor which was identified by probing lambda libraries of genomic		
CC DNA from a human monocytic-like cell line (U-60) and human peripheral		
CC blood lymphocytes using a large fragment of the interleukin-8 type		
CC A receptor DNA (See AAQ99006).		
XX		
Sequence 1737 BP; 454 A; 411 C; 373 G; 499 T; 0 other;		
XX		
Query Match	51.9%; Score 974.4; DB 16; Length 1737;	
Best Local Similarity	76.1%; Pred. No. 1.9e-174;	
Matches 1391; Conservative	0; Mismatches 301; Indels 136; Gaps 10	
OY 50 GCAGGTACGACGTACCCCTCTGAGGCGTTGGTGTCTCCGGTAACACACGCGCTAGAGAC		109
DB 20 GCGGGGCGCAAGATGACGCCGAGGCGCTGAGAGCTCCAGTACCCACCGCATCTGGAGAAC		79
OY 110 GAGGTGCCCATGAGACCGATCAGTGTAGTATTACACTTCTGGTAACCTACTCTGAAGA		169
DB 80 CAGCGTTACCATGGA-----GGGATACAGTATTATCACTTGAATATACACCGAGGA		134
OY 170 AGTGGGGCTCGAGACTATGATCCACAAAGGAACCTCTCTCCGGAGTGAAGAACGTCCA		229
DB 135 AATGGCGCTACGAGGAGCTATGACTCATGAAGGAACCGCTTTCCGGAAGAAAGTCPTAA		194
OY 230 TTTCATATGAGATCTTCCTGCGCACCATCTACTCTCATCTCTTCTGATGCGCATAGTCGG		289
DB 195 TTTCATATTAATCTTCCTGCGCACCATCTACTCTCATCTCTTCTTAAACGGGATTTGTGGG		254
OY 290 CAATGAGATGGTGCATCTGTCATGCGTTACACAGAAAGCTAAGAGCATACGAGACAA		349

Db	255	CAATGGATTGGTCAATCCGTGATCGGTTACGAGAAGAACTGGAAGCATGACGAGCA	314
OY	350	GTACCGGCTGCACTGTACGTAGTGGCTGACCTCTCTTTGTATATCAACTCCCTTCTGGGC	409
Db	315	GTACAGGGCTGACCGCTGACGTACAGTGGCGGACGCTCTTTGTCTATCAAGCTCTCCCTCTGGGC	374
OY	410	AGTTGATGCGCATGCTGACGTGATCTTTGGGAAATTTTGTGTAAAGCTGTCATATCAT	469
Db	375	AGTTGATGCCCTGGCAAACTGATCTTTGGGAACTTCTATGCAAGGACGTGATGATCAT	434
OY	470	CTACACTGTCAACCTCTACAGCAGCGTGTCTATCCTTGCCCTTTCATCAGCCTGGACCGGTA	529
Db	435	CTACACATCTCAACCTCTACAGCAGTGTCTATCCTTGCCCTTTCATCAGCCTGGACCGGTA	494
OY	530	CCTGGCCATTTTCCACGGCCACCAACAGTCAAGGCGCAAGGAAACTGGCTGGCTGAAAAGGC	589
Db	495	CCTGGCCATCTTCCACGGCCACCAACAGTCAAGGCGCAAGGAAACTGGCTGGCTGAAAAGGT	554
OY	590	AGCTATATGGGCGTTGGATCCGAGCCCTCTCTGATCTATTAACCTGACTTCATCTTTGCG	649
Db	555	GGTCTATGTTGGCGTGTGATCTCCCTGGCCCTCTGCTGTGATCTATCCGACCTTCATCTTTGCG	614
OY	650	CGAGCTAGCCAGGGGGGACATCATGTCAGGGGGATGACAGGTACATCTGTACGCCCTTTTA	709
Db	615	CAACG-----TCATGTAGGCGAGATGACAGATATCTGTGACGCCCTTTCTA	659
OY	710	CCCCGATAGCCTGTGATGATGATGATGATTTCAATTCAGCATATATGATGGTGGCTCATCTCT	769
Db	660	CCCCAATGATCTGTGGGGTGTGTGTGTTCATTTGACAGACATCATAGTTGGCCCTTATCTCT	719
OY	770	GCCCCGATCTCATCTCTCTCTCTGTACTGATATCATCTCTTAAGCTGTACACTCCA	829
Db	720	GCCGTGATTTATCATCTCTCTCTCTCTATGATTAATATCTCAAGCGTGTACACTCCA	779
OY	830	GGGCGACAGAAAGGCGCAAGGCCCTCAAGACACAGTATCCTCATCTGATCTTCTTTGCG	889
Db	780	GGGCGACAGAAAGGCGCAAGGCCCTCAAGACACAGTATCCTCATCTGCGCTTCTTTCGC	839
OY	890	CTGCTGCTGCATATTAATGTGGGGATCAGCATCGACTCTTTCATCTCTTTTGGAGTCAAT	949
Db	840	CTGTTGGCTGCTTACTCATTTGGGATTCAGCATCGACTCTTTCATCTCTCTGGAATCAT	899
OY	950	CACGAAAGATGTGATCTCGAGAGATGTGTCCAAAGGATGTTCATCAACAGAGGCCCT	1009
Db	900	CACGAAAGATGTGATCTCGAGAGATGTGTCCAAAGGATGTTCATCAACAGAGGCCCT	959
OY	1010	GCGCTTCTTCACATTTGCTCCGTAACCCCATCTCTATGCTCTCTCTCGGGGCGCAAGTTCAA	1069
Db	960	AGCTTTCTTCACATTTGCTGTGAACCCCATCTCTATGCTCTCTCTCGGGGCGCAAAATTTAA	1019
OY	1070	AAGCTTGTCCAGATGACATCACTCATATGAGACAGAGGCTCAGAGCTCAAGATCTTTTC	1129
Db	1020	AAGCTTGTCCAGATGACATCACTCTGTATGAGACAGAGGCTCAGAGCTCAAGATCTTTTC	1079
OY	1130	CAAGGAAAGCGGGGTGAGCACTCTTCGCTGTCCAGGAGTCAAAATCTCTGACATTTTCA	1189
Db	1080	CAAGGAAAGCGGGGTGAGCACTCTGTCTGTTCACAGTCAAGTCAAGTCTTCAAGTTTCA	1139
OY	1190	CTCAGACTAACCTTATGCAAGACTTATATATATATATATATATATATATATATGATTAAGACTT	1249
Db	1140	CTCAGACTTAA-----CACAGATGTAAAGACTTTTATATATATATATATATATATAT	1191
OY	1250	TTTATATGTTACATTTTCCAGATATAGACAGACAGCAGCTGTACAGTTTTTT	1309
Db	1192	TTTATATGTTACATTTTCCAGATATAGACAGACAGCAGCTGTACAGTTTATGTC	1251
OY	1310	TTTTTAATATGACTGTGGAGATTATATGTCTCTAGTTTGTGAGGTTTACTTAATTT	1369
Db	1252	TTGTTGGATTTTGT-----CTGTGTCTTTAGTTTGTGAGGTTTATATGACTTA	1305
OY	1370	ATATATATATTTGTTTGTGTTTGTTCATGTGAATGACGCTTACGACAGACCTGTGGCC	1429

Dd		1306	TTTTTAA-----TAATTTTTTTTTTGTTTCATATGATGATGTGGTCTAGGCAGACCGTGCC	136		
Oy		1430	AAGTTCCTTAGTACGTGTTTATCTGTGTGTAGACTGTAGAACCTAGACGAACAACCTGA	1489		
Dd		1362	AAGTTCCTTAGTGTGTATGCTGTGTGTAGACTGTAGAA-----AAGGAACTGA	1413		
Oy		1490	ACATTCCAGATGTGTGTAAATTGAATAAAGCTAGCCGTGATCCTCAGCTGTGTGCA	1549		
Dd		1414	ACATTCCAGACGCGTGTAGATCATACGTAAGCTAGAAATGATGCCACGCTTTATGCA	1473		
Oy		1550	TAAATCTCTCATTTCCGAGAGACCACCCACCCACCCACCCACCCCATTTCTTAAT	1609		
Dd		1474	TAGATTAATCTCTCCA-----	1488		
Oy		1610	TGTTTGGTATGCTGTGTGATGTTGTGTTGTTTTTTTTTGTTGTTGTTGTTTTT	1669		
Dd		1489	-----TTCCCCTGGAACGTTTTTCCCTGTTCTTATAGACGTGAT	1525		
Oy		1670	TTTTCTGTAAAGATGCGACCTTAAACCAAACCTGGAATGTGTGAGAAATGCTGGGT	1729		
Dd		1526	TTTCTGTGAGAAATGCGACCTTATAACCAAAAGCCCAAGTGGT-ATGAAATGCTGG--	1581		
Oy		1730	TTTTTTTGTTGTTGTTTTCAGTTTTCAGAGTATGATTGACTTCAGTCCCTACAAT	1789		
Dd		1582	-----TTTTTCAGTTTTCAGGAGTGGGTGTGATTTTACGACCTCAC-Agt	1623		
Oy		1790	GTCACGCTTGTATTACATTTGTATTAAGTCAATGATTAACCTTAAAAAAA	1849		
Dd		1624	GTCACGCTTGTATTAGTTGTATTAAGTACATGTTAACCTTAAAAAAA	1683		
Oy		1650	AAAAAAAAAAAAAAAAAAAAAA 1877			
Dd		1684	AAAAAAAAAAAAAAAAAAAAAA 1711			
<hr/>						
RESULT_5						
ID	AAQ29506	standard; DNA; 1737 BP.				
XX	AAQ29506;					
XX	DT	12-MAR-1993	(first entry)			
XX	DE	New platelet factor 4 receptor superfamily member PF4ARI.				
XX	KW	IL-8R; G-protein coupled receptor family; rhodopsin superfamily;				
KW	pro-inflammatory cytokine; 8rf.20.15; ss.					
OS	Homo sapiens.					
XX	Key	Location/Qualifiers				
FT	CDS	91..1149	/tag= a			
FT		/product= PF4ARI				
XX	PN	W09217497-A.				
XX	PD	15-OCT-1992.				
XX	PE	23-MAR-1992;	92WO-USO2317.			
PR	29-MAR-1991;	91US-0677211.				
PR	19-DEC-1991;	91US-0810782.				
PA	(GETH) GENENTECH INC.					
PI	Holmes WE, Lee J, Wood WI;					
DR	WPI: 1992-366191/44.					
DR	P-PSDB: AAR27792.					
PT	Isolated human platelet factor 4 super-family receptor					
PT	polypeptide and corresp. antibodies and DNA - useful as					

PT diagnostic and screening agents, and for treating inflammation or
PFAR-mediated disorders

PS Claim 7; Fig 4; 78pp; English.

CC The IL-8 receptor cDNA sequence was isolated (see AA029505) and a
CC 874bp sub-fragment of the coding sequence was used as a probe to
CC screen human cell line HL60 and human peripheral blood lymphocyte
CC cDNA libraries. Two new gene sequences were found that are clearly
CC related to the IL-8 receptor. One of these was contained in
CC combined clone 8tr.20.15 and is predicted to encode an amino acid
CC sequence which is 34% identical with both the high and low affinity
CC IL-8 receptors. See also AA037107.

XX Sequence 1737 BP; 457 A; 412 C; 370 G; 498 T; 0 other;

Query Match 51.7%; Score 969.6; DB:13; Length 1737;
Best Local Similarity 75.9%; Pred. No. 1.5e-173;
Matches 1388; Conservative 0; Mismatches 304; Indels 136; Gaps 10;

50 GCAGGTAGACAGTACCTCTGAGCGCTTGTGCTCCGCTAACCCAGCGCTGAGAGC 109
11
20 GCGGGGGGCAAGAGAGAGCGGAGGCGCTGAGTGCCTCCAGTAGCCAGCCGATCTGAGAAC 79
110 GAGTGTGGCATGGAACCGATCACTGTGATATATACACTTCTGATTAAGTCTGAGA 169
80 CAGCGGTATACATGGA-----GGGATACAGTATATACCTTCAGATATACCTACCGAGA 134
170 AGTGGGTGTGAGACATATGATCTCCAAAGAAAGCCCTGCTCCGGGATGAAACGTCCA 229
135 AATGGGTGTGAGAGGAGATGATGATCAATGAAGAAAGCCCTGCTCCGGGATGAAACGTCCA 194
230 TTTCATAGATATCTCTCCGCGCCACCATCTACTCTATCATCTTCTGATTAAGTCTGAGA 289
195 TTTCATAGATATCTCTCTCCGCGCCACCATCTACTCTATCATCTTCTGATTAAGTCTGAGA 254
290 CAATGATATGATGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 349
255 CAATGATATGATGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 314
350 GTACGGGTGACCTGTCAGAGGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 409
315 GTACAGGTGACCTGTCAGAGGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 374
410 AGTGTATGATGATGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 469
375 AGTGTATGATGATGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 434
470 CTACAGGTGACCTGTCAGAGGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 529
435 CTACAGGTGACCTGTCAGAGGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 494
530 CCTGCGCATGTCACCGCCACCAACAGTCAAGAGGCAAGAACTGCTGCTGAAAGGC 589
495 CCTGCGCATGTCACCGCCACCAACAGTCAAGAGGCAAGAACTGCTGCTGAAAGGC 554
590 AGTGTATGATGATGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 649
555 GGTATGATGATGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 614
650 CGAGGTGACCGAGGAGGAGATCACTGATGAGGAGGATGAGATGATGATGATGATGATGAT 709
615 CAAAG-----TCACTGAGGAGGAGATGATGATGATGATGATGATGATGATGATGAT 659
710 CCGCGATAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 769
660 CCGCGATAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 719
770 GCGCGATAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 829
720 GCGCGATAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 779
830 GCGCGATAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 889

||||| 780 GGGCCACGAGAGGCAAGGCCCTCAAGACCAAGTATCTCTGCTGCTTCTTCCG 839
890 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 949
840 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
950 CAACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1009
900 CAACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 959
1010 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1069
960 AGCTTCT 1019
1070 AAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1129
1020 AAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079
1130 CAACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1189
1080 CAACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1139
1190 CTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1249
1140 CTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1191
1250 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1309
1192 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1251
1310 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1369
1252 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1305
1370 AATATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1429
1306 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1361
1430 AAGCTTCT 1489
1362 AAGCTTCT 1413
1490 ACATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1549
1414 ACATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1473
1550 TATATCT 1609
1474 TAGATATCT 1488
1610 TGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1669
1489 -----TTCCGTTGGAAGGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1525
1670 TTTTCTGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1729
1326 TTTTCTGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1581
1730 TTTTCTGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1789
1582 -----TTTCTGATGTTTGAAGTGGTGGTGAATTCAGACCTAC-AGT 1623
1790 GTACAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1849
1624 GTACAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1683
1850 AAAAAAAAAAAAAAAAAAAAAAAAAA 1877
1684 AAAAAAAAAAAAAAAAAAAAAAAAAA 1711

AA165467
ID AA165467 standard; DNA: 1679 BP.
AC AA165467:
XX
XX
XX 10-DEC-2001 (first entry)
XX
XX Nucleotide sequence of a human polynucleotide.
XX
XX Human: receptor: DC-SIGN; dendritic cell; T lymphocyte; HIV;
XX gp120; C-type lectin; ICAM3; HIV entry; T cell; macrophage;
XX HIV infection; ss.
XX Homo sapiens.
XX OS
XX WO200164752-A2.
XX
XX 07-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US06322.
XX
XX 02-MAR-2000; 2000US-0517605.
XX
XX (UYNV) UNIV NEW YORK STATE.
XX (UYNV) UNIV NIJMEGEN.
XX
XX Litman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;
XX WPI: 2001-602565/68.
XX
XX An antibody for the treatment or prevention of HIV-infection comprises
XX a gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding
XX of DC-SIGN due to concomitant conformational change -
XX
XX Disclosure: Page 126-127; 131pp; English.
XX
XX The specification describes an antibody which is specific for an
XX antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN
XX or is exposed upon gp120 binding of DC-SIGN due to concomitant
XX conformational change. DC-SIGN is a receptor that is specifically
XX expressed on dendritic cells and facilitates infection of T lymphocytes
XX with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin.
XX DC-SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
XX with high affinity. The antibody of the invention inhibits the trans
XX enhancement of HIV entry into a T cell or macrophage facilitated by
XX dendritic cells. The antibody is useful to treat or prevent HIV
XX infection. The present sequence represents a human polynucleotide,
XX which is used in the course of the invention.
XX
XX Sequence 1679 BP: 407 A; 400 C; 368 G; 504 T; 0 other:
XX
XX Query Match 50.8%; Score 952.8; DB 22; Length 1679;
XX Best Local Similarity 80.2%; Pred. No. 2.2e-170;
XX Matches 1210; Conservative 0; Mismatches 252; Indels 46; Gaps 6;

247 TGTGGCAATGATTTGGTCACTCTGATCGATGGTTACCAAGAACTGAAAGCATGAC 306
344 GGACAAATGACGGGTGACACTGTGACAGTGGCTGACCTCTTTGTATCATCACTCCCTT 403
307 GGACAAATGACGGGTGACACTGTGACAGTGGCTGACCTCTTTGTATCATCACTCCCTT 366
404 CTGGGAGTTGATGCTGACCTGACCTGATCTTTGGGAAATTTTGTAAAGCTGTGCA 463
367 CTGGGAGTTGATGCTGACCTGACCTGATCTTTGGGAAATTTTGTAAAGCTGTGCA 426
464 TATCATCTACACTGTCAACCTGTACAGACAGTGTCTATCCTGGCTTCATCACTGCA 523
427 TGTATCTACAACTGCAACCTGTACAGAGTGTCTATCCTGGCTTCATCACTGCA 486
524 CCGGTACCTGGCTGATGTCACAGCCACCAACAGTCAAGGCAAGCAACTGCTGGCTGA 583
487 CCGGTACCTGGCTGATGTCACAGCCACCAACAGTCAAGGCAAGCAACTGCTGGCTGA 546
584 AAAGCAGTCTATGTCGCTGATGTCACAGCCCTCTGCTGATCTTACCTGATCTCAT 643
547 AAAGTGTGCTATGTCGCTGATGTCACAGCCCTCTGCTGATCTTACCTGATCTCAT 606
644 CTTTGGCAGTCAAGCCAGGGGACATCACTCAAGGGGATGACAGTACATCTGTGACG 703
607 CTTTGGCAGTCAAGCCAGGGGACATCACTCAAGGGGATGACAGTACATCTGTGACG 651
704 CTTTACCCGATGATGCTGATGTCAGTGGTGTTCATCTCCAGATATATGTTGGTCT 763
652 CTTTACCCGATGATGCTGATGTCAGTGGTGTTCATCTCCAGATATATGTTGGTCT 711
764 CACTCTCCGCGGCTGATGCTGATGTCAGTGGTGTTCATCTCCAGATATATGTTGGTCT 823
712 TATCTGCTGATGTCAGTGGTGTTCATCTCCAGATATATGTTGGTGTTCATCTCCAG 771
824 CTCCAAAGGCGCCAGAGGCGCAAGGCTCAAGACAGTCACTCTCATCTGCTT 883
772 CTCCAAAGGCGCCAGAGGCGCAAGGCTCAAGACAGTCACTCTCATCTGCTT 831
884 CTTTGGCAGTCAAGCCAGGGGACATCACTCAAGGGGATGACAGTACATCTGTGACG 943
832 CTTTGGCAGTCAAGCCAGGGGACATCACTCAAGGGGATGACAGTACATCTGTGACG 891
944 AGTCAAGCAAGATGATGATGTCAGAGATGTCAGAGATGTCAGAGATGTCAGAGAT 1003
892 AATCATCAAGCAAGATGATGATGTCAGAGATGTCAGAGATGTCAGAGATGTCAGAG 951
1004 GGGCTGCTGCTTCTTCACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1063
952 GGGCTGCTGCTTCTTCACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1011
1064 GTTCAAAAGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1123
1012 ATTAAAGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1071
1124 CTTTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1183
1072 CCGTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1131
1184 TTTTCACTCAAGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1243
1132 TTTTCACTCAAGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1183
1244 GAATTTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1303
1184 ACTTTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1243
1304 TTTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1363
1244 TATGCTGTTGATTTTGTG-----CTTGTGTTTGTAGTTTGTGAAGTTTATTT 1297
1364 TAAATTTATTAATATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1423
1298 GACTTATTTATA-----TAAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1353


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OY 1064 GTTCAAAAGCTCTGCCAGCATGACATCACTCACTGACAGAGAGGCTCCAGCTCAAGAT 1123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1012 ATTTAAACCTCTGGCCAGCAGCAGCACTCTCTGTGAGCAGAGGGTCCAGCTCAAGAT 1071
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1124 CCTTTCAGAGAAAGCGGGGCGGAGACTCTTCCGCTCCAGGAGTCAAGATCTCCAG 1183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1072 CCTCTCCAAAGAAAGCGAGGAGGATCTCTGTTCCAGTGTGAGCTCTTCAAG 1131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1184 TTTTACCTCAGCTAACCTTATGCAAGATATATATATATATATATATATATATATAT 1243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1132 TTTTACCTCAGCTAACATGATATATATATATATATATATATATATATATATATAT 1183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1244 GAATTTTATATATATATATATATATATATATATATATATATATATATATATATAT 1303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1184 ACTTTTATATATATATATATATATATATATATATATATATATATATATATATATAT 1243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1304 TTTTATTTTATATATATATATATATATATATATATATATATATATATATATATAT 1363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1244 TATTCCTGCTGATATATATATATATATATATATATATATATATATATATATATAT 1297
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1364 TATTTATATATATATATATATATATATATATATATATATATATATATATATATAT 1423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1298 GACTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1353
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1424 GTGGCCAGCTCTTATATATATATATATATATATATATATATATATATATATATAT 1483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1354 GTGGCCAGCTCTTATATATATATATATATATATATATATATATATATATATATAT 1405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1484 AACTGAACTTCCAGATATATATATATATATATATATATATATATATATATATATAT 1543
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1406 AACTGAACTTCCAGATATATATATATATATATATATATATATATATATATATATAT 1465
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1544 GCTGCATA 1551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1466 TATGCATA 1473
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
AAA61656
ID AAA61656 standard; DNA; 1664 BP.
XX
AC AAA61656;
XX
DT 23-OCT-2000 (first entry)
XX
DE Human CXCR4 chemokine receptor (CXCR4) cDNA.
XX
KW CXCR4; human CXCR4 chemokine receptor 4; HIV infection inhibition;
expression inhibition; antisense therapy; ss.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH primer_bind 67..80
FT /tag= a
FT /bound_moiety= "Antisense oligonucleotide SEQ ID NO:1"
FT primer_bind 73..96
FT /tag= b
FT /bound_moiety= "Antisense oligonucleotide SEQ ID NO:2"
FT primer_bind 61..83
FT /tag= b
FT /bound_moiety= "Antisense oligonucleotide SEQ ID NO:3"
XX
XX WO2000031271-A1.
XX
XX 02-JUN-2000.
XX
XX 24-NOV-1999; 99WO-JP06534.
XX
XX 24-NOV-1998; 98JP-0332760.
```

```
XX (HISM ) HISAMITSU PHARM CO LTD.
PA Iijima O, Goto T, Shimada T;
PI WPI: 2000-400081/34.
XX
DR Antisense oligonucleotide, useful as inhibitor in preventive or remedy
PT for HIV infection with high therapeutic efficacy
XX Example 1; Page 17-18; 21pp; Japanese.
PS
XX
XX The invention relates to human CXCR4 chemokine receptor 4 (CXCR4)-specific
CC antisense oligonucleotides (AAA61652-AAA61654). The oligonucleotides
CC hybridise with the CXCR4 gene and/or CXCR4 RNA, thereby preventing its
CC expression. As CXCR4 plays a role in HIV infection, the antisense
CC oligonucleotides act as inhibitors of this process. Compositions
CC containing the antisense oligonucleotides are useful as prophylactic
CC or therapeutic agents for HIV infection. Such compositions are highly
CC efficacious for inhibiting infection with HIV. The present sequence
CC represents a human CXCR4 cDNA.
SQ Sequence 1664 BP; 414 A; 398 C; 359 G; 493 T; 0 other;
Query Match 50.7%; Score 951.8; DB 21; Length 1664;
Best Local Similarity 80.2%; Pred. No. 3.4e-170;
Matches 1209; Conservative 0; Mismatches 252; Indels 46; Gaps 6;
OY 45 CAGGTGCAAGTATGACAGTACCTCTGAGGCGTTTGCTCGGTAACACCGAGCTGT 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 CGGACAGAGTATGACAAAGTACCGAGGCGCTGAGTGTCTCAGTACGACCGCATCTGG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 105 ACAGGAGATGTGCGCATGGAACCGATCAAGTATATATATATATATATATATATATATAT 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 AGAACACAGCGCTTACATATGA-----GGGATCAATATATATATATATATATATATAT 115
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 165 GAAGAAGTGGGCTGTGAGACTATGATCTCAACAAAGAACCCCTGCTCCGGATGAAG 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 116 GAGGAATATGGGCTCAGGGAGATATGATCCATGAGAAACCTGTTCGGTGAAGAAAT 175
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 225 GTTCATTTCAATATATATATATATATATATATATATATATATATATATATATATAT 284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 176 GCTAATTTCAATATATATATATATATATATATATATATATATATATATATATATAT 235
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 285 GTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 344
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 236 GTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 295
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 345 GACAAATGACGCGTACACCTGTCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 404
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 296 GACAAATGACGCGTACACCTGTCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 355
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 405 TGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 464
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 356 TGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 415
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 465 ATCATCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 416 GTCATCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 475
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 525 CGGTACCTGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 584
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 476 CGGTACCTGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 535
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 585 AAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 644
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 536 AAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 595
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 645 TTTGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 704
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 596 TTTGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 640
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 705 CTTTACCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 764
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db      641 TTCTACCCCAATGCTGTGGGTGGTGTGTTGCTGAGTTCAGACATCATGTTGGCTT 700
QY      765 ATGCTGGCCGGGATTCGATCCCTCTCTCTGTACTGATCATCTCTAAGCTGTACAC 824
Db      701 ATCTGCTGTGGTATGTCATCTCTCTCTCTGTATGATATATATCAAGCTGTACAC 760
QY      825 TCCAAAGGCGCAGAGAGCCAGAGCCCTCAAGACGACATCATCTCTAGCTTTC 884
Db      761 TCCAAAGGCGCAGAGAGCCAGAGCCCTCAAGACGACATCATCTCTAGCTTTC 820
QY      885 TTTGCTGTGCTGTGCTGCTATATATGTTGGGATCAGACATCTCTCTAGCTTTC 944
Db      821 TTGCTGTGCTGTGCTGTGCTATATGTTGGGATCAGACATCTCTCTAGCTTTC 880
QY      945 GTATCAAGCAGAGAGTGTGCTGTGAGAGATCTGTGAGACATCTCTCTAGCTTTC 1004
Db      881 ATATCAAGCAGAGAGTGTGAGAGTGTGAGACATCTGTGAGATCTCTCTAGCTTTC 940
QY      1005 GCCCTGCGCTTCTTCCAGCTGTGCTGTGAGAGCCATCTGTATGCTCTCTGAGGCGCAG 1064
Db      941 GCCCTGAGCTTCTTCCAGCTGTGCTGTGAGAGCCATCTGTATGCTCTCTGAGGCGCAG 1000
QY      1065 TTCAAAAGCTCTGCGCAGAGATGACATCACTGATGAGAGAGGCTCTCAAGATC 1124
Db      1001 TTAAAGCTCTGCGCAGAGATGACATCACTGATGAGAGAGGCTCTCAAGATC 1060
QY      1125 CTTTCCAAAGGAGAGGAGGAGTGTGAGACATCTCTGCTCTCCAGAGTCAAGATCTCTCAGT 1184
Db      1061 CTCTCCAAAGGAGAGGAGTGTGAGACATCTCTGCTCTCCAGAGTCAAGATCTCTCAGT 1120
QY      1185 TTTTACCTCAGATACCTTATGCAAGAGCTTATATATATATATATATATATATATAG 1244
Db      1121 TTTTACCTCAGATACCTTATGCAAGAGCTTATATATATATATATATATATATATAG 1172
QY      1245 AACTTTTATATGTTACATATTTTCCAGATATATAGAGAGTCAAGATCTCTTACAGTTT 1304
Db      1173 CTTTATTTTAAAGTTACATATTTTCCAGATATATATATATATATATATATATAGTTT 1232
QY      1305 TTTTATTTTAAATGAGCTGTGAGAGTGTATGTTCTCTGATGTTTGTGAGGTTTGCCT 1364
Db      1233 ATGCTGTGTGAGATTTTGTG-----CTGTGTGTTTCTTGTGATTTTGTGAGGTTTATG 1286
QY      1365 AATTATATATATATGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 1424
Db      1287 ACTTATTTATA-----TAAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 1342
QY      1425 TGGCCAAAGTCTTATAGTGTGTTTATCTGTGTGAGAGTGTGAGACTGTAGAGAGAA 1484
Db      1343 TGGCCAAAGTCTTATAGTGTGTTTATCTGTGTGAGAGTGTGAGACTGTAGAA-----AAGGA 1394
QY      1485 ACTGAAGATTCGAGATGTGTGTAATTAATTAAGAGTGTGAGAGTGTGAGAGTGTG 1544
Db      1395 ACTGAAGATTCGAGAGTGTGTAATTAATTAAGAGTGTGAGAGTGTGAGAGTGTG 1454
QY      1545 CTGAGATA 1551
Db      1455 ATGATTA 1461

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RESULT 9
AAZ40014
ID AAZ40014 standard; DNA: 1664 BP.

XX AAZ40014;

XX 14-FEB-2000 (first entry)

XX CXCR4 coding sequence.

XX CXCR4, inhibitor; antisense oligonucleotide; anti-HIV agent;

KW HIV infection; therapy; ss.

XX

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OS      Synthetic.
XX      JP11285391-A.
PN      19-OCT-1999.
XX      18-NOV-1998; 98JP-0327942.
XX      19-NOV-1997; 97JP-033085.
PA      (HISM ) HISAMITSU PHARM CO LTD.
PA      (TOAG ) TOA GOSSEI CHEM IND LTD.
DR      WPI; 2000-026817/03.
XX      An oligonucleotide used as an anti-HIV agent - inhibits CXCR4 protein
PT      expression
PT      expression
XX      Disclosure; Page 5-6; 6pp; Japanese.
PS      This sequence represents a CXCR4 coding sequence. The invention relates
CC      to antisense oligonucleotides that hybridise specifically with
CC      chromosomal DNA and/or RNA encoding a CXCR4 protein, and inhibit the
CC      expression of the CXCR4 protein. The antisense oligonucleotides can be
CC      used in an anti-HIV agent. The oligonucleotides and the anti-HIV agent
CC      are highly effective as a preventive and treating agent for HIV
CC      infection.
XX      Sequence: 1664 BP; 414 A; 398 C; 359 G; 493 T; 0 other;
SQ
QY      45 CAGGTGAGGTAGCAGTACGACCTCTGAGGCGTTTGTGCTCGGTATACACACAGCGCTGT 104
Db      1 CGGAGCAGAGGTAGCAAGATGACGCGGAGGCTGAGTGTCTGACGTACACCGCATGTG 60
QY      105 AGAGCGAGTGTGCGATGAGAACCGATCATGTGTATATACCTGTGTATCTACTCT 164
Db      61 AGAACCGAGGCTTACATGGA-----GGGATCATGATATATACCTGTATATACATAC 115
QY      165 GAAGAGTGGGCTGTGAGACTATGACTCCAAAGACCTCTGCTCCGGATGAAG 224
Db      116 GAGAAATGGGCTGTAGGAGTATGACTCCATGAGAGAACCTCTGCTCCGGATGAAG 175
QY      225 GTCCATTTCAATAGATCTTCTGCTGCCACCATCTACTTCAATCTTCTTACTGAGCATA 284
Db      176 GTATATTTCAATATTAATCTTCTGCTGCCACCATCTACTTCAATCTTCTTACTGAGCATT 235
QY      285 GTGGCAATGATTTGTGATCTGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATG 344
Db      236 GTGGCAATGATTTGTGATCTGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATG 295
QY      345 GACAAATGAGGCTGTGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAG 404
Db      296 GACAAATGAGGCTGTGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAG 355
QY      405 TGGGCAATGATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATG 464
Db      356 TGGGCAATGATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATG 415
QY      465 ATCATCTACATGTGCAAGCTCTTACAGAGGTTTCTATCTGAGCTTCTACAGCTGTGAC 524
Db      416 GTCATCTACATGTGCAAGCTCTTACAGAGGTTTCTATCTGAGCTTCTACAGCTGTGAC 475
QY      525 CGTACCTGCGCATTTGCCAGCGCACCAAGATCAAGATCAAGATCAAGATCAAGATCAAG 584
Db      476 CGTACCTGCGCATTTGCCAGCGCACCAAGATCAAGATCAAGATCAAGATCAAGATCAAG 535
QY      585 AAGGAGTCTATGTGGGCTGTGAGTCCAGGCTCTCTGCTGAGTATCTGAGTATCTGATC 644
Db      536 AAGGAGTCTATGTGGGCTGTGAGTCCAGGCTCTCTGCTGAGTATCTGAGTATCTGATC 595

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OY	645	TTTTCCGACGTCACGACGAGGGGACATCAGCTCAGGCGGATGACAGTACATCTGTGACCG	704
Db	596	TTTTGGCAACG-----TCAGTAGCGAGATGACAGATATATCTGTGACCGC	640
OY	705	CTTTACCCCGCATACCTGTGGATGGTGGTGTGTTTCAATTCACGCAATATATGGTGGCTTC	764
Db	641	TTTACACCCCATGACTGTGGGTGGTGTGTTCAGATTTCAGACATCATGTGGTGGCCTT	700
OY	765	ATCCTGCCCCGATCTGCTATCCCTCTCTGTTACTGCATCATCATCTTAAGCTGTGCACAC	824
Db	701	ATCCGCTGGATATGTTCATCTCTGCTCCGCTATTGCAATTATCATCTCCAACTGTGCACAC	760
OY	825	TCGAAGGCGCACGAAAGCGAAGGCCCTCAAGACGACAGTATCTCATCTGTGCTTC	884
Db	761	TCGAAGGCGCACGAAAGCGAAGGCCCTCAAGACGACAGTATCTCATCTGTGCTTC	820
OY	885	TTTGCTGCTGCTGCTCCATATATATGTTGGGATGTCAGCATCGACTCTTCATCTTTTGGA	944
Db	821	TTTGCTGCTGCTGCTCCATATATGTTGGGATGTCAGCATCGACTCTTCATCTTTTGGA	880
OY	945	GTATATCAAGCAAGATGTGACTTGCAGAGCATTTGTCACAAAGTGATCTCCATCCAGAG	1004
Db	881	ATCATCAAGCAAGGCTGTGAGTTTGAGAACACTGTGCACAAGTGATTTCCATCACCGAG	940
OY	1005	GGCCGCGCTCTTCCACTGTGTGCTGAAACCCCATCTTATGCTTCCTGGGGCCAG	1064
Db	941	GGCCGCTCTTCTTCCACTGTGTGCTGAAACCCCATCTTATGCTTCCTGGGGCCAA	1000
OY	1065	TTCAAAAGCTGTGCCACAGCATGACACTCACTCACTCAGACAGAGGCTCCAGCTCAAGATC	1124
Db	1001	TTTAAACCTGTGCCACAGCATGACACTCACTCTGTGACACAGAGGCTCCAGCTCAAGATC	1060
OY	1125	CTTTCCAAAGAAAGCGGGGTGAGACTCTTCCGCTCTCCACGAGTCAAGATCTCCAGT	1184
Db	1061	CTCTCAAGGAAAGCGAGGTGAGACTCATCTGTTTCCACTGAGTCTGAGCTTCAAGT	1120
OY	1185	TTTCACTACACTAACCTTATGCAAGAACTATATATATATATATATATATATGATAAG	1244
Db	1121	TTTCACTACACTAACCTTATGCAAGATGTAAGAACTTTT-----TTTATGAGATATAATA	1172
OY	1245	AACATTTTATGTTACACATTTTCCAGATATAGAGACTGCACAGCTTGTACAGTTTTT	1304
Db	1173	CTTTTATTAAGTTACACATTTTCCAGATATAGAAAGACTGCACAAATATGTACAGTTTTT	1232
OY	1305	TTTTTTTATTAATGACTGTGGAGATTATGTTCTCTAGTTTTTGTGAGCTTGTGACTT	1364
Db	1233	ATTTGCTGCTGAGATTTTGT-----CTTGTGTTTCTTATGTTTTTGTGAAGTTTAATTTG	1286
OY	1365	AATTTATTAATAATATGTTTTTTTGTGTTTTCATAGTGAATGAGGCTCAGAGAGACTGT	1424
Db	1287	ACTTATTTATA-----TAATTTTTTTTGTGTTTTCATATGATGTGTGTAGAGAGAGACTGT	1342
OY	1425	TGGCCAAAGTTCTTAGTAGCTGTTATATCTGTGTAGAGACTGTAGAACTGTAGAGAAAG	1484
Db	1343	TGGCCAAAGTTCTTAGTAGCTGTATGTCTCGTGTGTAGAGACTGTAGAA-----AAGGA	1394
OY	1485	ACTGAACATTCAGAAATGTGTGTAATTTGAATAAGCTAGCCGATCTCAGCTGTTG	1544
Db	1395	ACTGAACATTCAGAGCGTGTAGTTAATCACGTAAGCTAGAAATGATCCAGCTGTTT	1454
OY	1545	CTGCATA 1551	
Db	1455	ATGCATA 1461	

RESULT	10
	ABK83803
ID	ABK83803 standard; cDNA; 1670 bp
XX	
AC	ABK83803;
XX	
DT	14-AUG-2002 (first entry)

DE Human cDNA differentially expressed in granulocytic cells #374.
XX
XX
KW Human; ss: granulocytic cell; DNA chip; bacterial infection;
XX viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
XX Homo sapiens.
OS
PN MO200228999-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001MO-US30821.
XX
PR 03-OCT-2000; 2000US-237189P.
XX
XX (GENE-) GENE LOGIC INC.
PA
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR WPI: 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
XX drug toxicity
PS
PS Claim 1: SEQ ID NO 374; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1670 BP: 418 A; 400 C; 361 G; 491 T; 0 other;

Query Match 50.3%; Score 944.8; DB 24; Length 1670;
 Best Local Similarity 75.9%; Pred. No. 7,1e-169;
 Matches 1356; Conservative 0; Mismatches 297; Indels 133; Gaps 10;

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OY 66 CTGTGAGGCGTTTGGTCTCGGTAAACACACAGGCGTGTAGAGCGAGTGTGGCATGAA 125
Db 18 CGCCGAGGCGCGTAGGTCTCGAGTGCACCGCATCTGAGAAACAGCGGGTTACCATGGA 77
OY 126 CCGATCAGTGTGAGTATATACACTTCTATACCTCTGTGAAGAAGTGGGCTGTGAAC 185
Db 78 -----GGGGATCAGATATATACACTTCAACATACACCGAGGAAGGGCTCAGGGAC 132
OY 186 TATGATCCACAAGAACCCCTGCTCCGGATGAAAGCGTCATTTTGAATAGATCTTC 245
Db 133 TATGATCTCATGAAAGAACCTGTTCCGTGAGAAAGTGCATATTTAATAAATCTTC 192
OY 246 CTGCCCCACATCTACTTCATCATCTTCTGACTGGCATAGTCGGCAATGGATGGTGATC 305
Db 193 CTGCCACCATCTACTCCATCATCTTCTTAACCTGSCATGTGGCAATGGATGGTGATC 252
OY 306 CTGTGCATGGGTTACCAAGAAGTAAAGACATGAGACAGTACCAGCTGCACCTG 365
Db 253 CTGTGCATGGGTTACCAAGAAGTAAAGACATGAGACAGTACCAGCTGCACCTG 312
OY 366 TCAGTGGCGTGAACCTCTTGTGTCACACCTCCCTCTGGGCGATTGATGCCATGGT 425
Db 313 TCAGTGGCGGACCTCTCTTGTGTCACACCTCCCTCTGGGCGATTGATGCCATGGT 372
OY 426 GACTGTACTTGGGAAATTTTGTGTAGGCTGTGCATATCATCTACACTGTCAACCTC 485
Db 373 AACTGTACTTGGGAAATTTTGTGTAGGCTGTGCATATCATCTACACTGTCAACCTC 432
OY 486 TACACACAGCTTCTATCTCGGCTTTCATCAGCTGAGACCGGTACCTGGCCATTGTCCAC 545
Db 433 TACACACAGCTTCTATCTCGGCTTTCATCAGCTGAGACCGGTACCTGGCCATTGTCCAC 492
OY 546 GCCACCAACAGTCAAGGCGCAAGAACTGCTGGGTGAAGAGCGAGTGTATGTGGGCTC 605
Db 493 GCCACCAACAGTCAAGGCGCAAGAACTGCTGGGTGAAGAGCGAGTGTATGTGGGCTC 552
OY 606 TGGATCCAGCCCTCTCTCTGACATATCTGATCTTCATCTTCCGACGTCAGCCAGGGG 665
Db 553 TGGATCCCTGCTCTCTCTGACATATCTGATCTTCATCTTCCGACGTCAGCCAGGGG 601
OY 666 GACATCATCAGGGGAGTGAAGATGATCTGTGACCCGCTTACCAGCATAGCTGTGG 725
Db 602 ----TCAGTGAAGGCGATGACAGATATCTGTGACCCGCTTACCCCAATGACTTGGG 657
OY 726 ATGTGTGTCTTCAATTCACAGCATATATGATGGGTCTCATCTCCGCGCATCTCATC 785
Db 658 GTGGTGTGTCTCAATTCACAGCATATATGATGGGTCTCATCTCCGCGCATCTCATC 717
OY 786 CTCTCTCTTACTGATCATCTCTTAAGCTGTCACTCCAGGCGCACCAAGAGCGC 845
Db 718 CTGTCTCTCTTACTGATCATCTCTTAAGCTGTCACTCCAGGCGCACCAAGAGCGC 777
OY 846 AAGGCGCTCAAGAGACAGTATCTCTCAAGTCTTCTTCTGCTGTGGCTGCTTAC 905
Db 778 AAGGCGCTCAAGAGACAGTATCTCTCAAGTCTTCTTCTGCTGTGGCTGCTTAC 837
OY 906 TATGTGGGATCAGCATGACTCTTCAATCTTGGGAGTCAATAGCAAGAGTGTAC 965
Db 838 TACATTTGGGATCAGCATGACTCTTCAATCTTGGGAGTCAATAGCAAGAGTGTAG 897
OY 966 TTTCGAGACATTTGTCACAGTGTATCTTCATCAGAGAGCGCTGCTTCTTCCACTGT 1025
Db 898 TTTCGAGACATTTGTCACAGTGTATCTTCATCAGAGAGCGCTGCTTCTTCCACTGT 957
OY 1026 TGCCGTAAGCCCATCTCTATGCCCTCTCCGGGCGCAAGTTAAAGCTTCCCGACAT 1085
Db 958 TGTCTGAACCCCATCTCTATGCTTCTTCTGGAGCAAAATTTAAACCTGTGCCAGCAC 1017

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OY 1086 GCACCTCACTCCATGAGCAGAGGCTCCAGCCCTCAAGATCTTCCAAAGAAAGCGGGT 1145
Db 1018 GCACCTCACTCTGTGTAGAGAGGCTCCAGCCCTCAAGATCTTCCAAAGAAAGCGAGT 1077
OY 1146 GCACCTCTCCGCTCCAGCAGGATGACAAATCTCCAGTTTCTACCTCAGCTAACCTTAA 1205
Db 1078 GCACCTCACTCTGTGTAGAGAGGCTCCAGCCCTCAAGATCTTCCAAAGAAAGCGAGT 1131
OY 1206 TGCAAGACTATATATATATATATATATATATATATATATATATATATATATAT 1265
Db 1132 --CAGAGATGAAGAGACTTTTATATATATATATATATATATATATATATATAT 1189
OY 1266 TTCCAGATATGAAGAGACTGACAGCTCTGTACAGTTTCTTCTTCTTCTTCTTCTTCT 1325
Db 1190 TTTCAGATATATGAAGAGACTGACAGCTCTGTACAGTTTCTTCTTCTTCTTCTTCTTCT 1245
OY 1326 GGGAGTTATATGCTCTAGTTTCTTGTAGGTTTGTGAGTTTGTGAGTTTGTGAGTTT 1385
Db 1246 TGTCTCTGTGTTCTTGTAGTTTGTGAGTTTGTGAGTTTGTGAGTTTGTGAGTTTGTGAG 1302
OY 1386 TTGTTGTTTCTATGTGATGAGACCTCTGAGCAGACCTGTGGCCAGTTCTTACTAGCTG 1445
Db 1303 TTTTGTGTTTCTATGTGATGAGACCTCTGAGCAGACCTGTGGCCAGTTCTTACTAGCTG 1362
OY 1446 TTTATCTGTGTAGACTGTGAGACTGTGAGAGAAAGTGAAGTTCAGATTCAGATTCGT 1505
Db 1363 TATGTCTGTGTGTAGACTGTGAGACTGTGAGAGTTCAGATTCAGATTCGT 1414
OY 1506 GGTAAATTTGAATGAAGTACAGCCGTGATCTGACCTGTGTCGATATATCTTCATTCG 1565
Db 1415 AGTGAATCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1473
OY 1566 AGGACACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCC 1625
Db 1474 ----- 1473
OY 1626 GTGATGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 1685
Db 1474 -----TTCCGCTGAGAACGTTTTCCTGTTCTTAAAGACGATTTTCTGTGAGAGATG 1526
OY 1686 GCACCTTAAGAACCAAGCCTGAAGTGTGAGTGAAGTGTGAGTGTGAGTGTGAGTGTGAG 1745
Db 1527 GCACCTTAAGAACCAAGCCTGAAGTGTGAGTGAAGTGTGAGTGTGAGTGTGAGTGTGAG 1566
OY 1746 TTTTTCAGTTTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1805
Db 1567 -TTTTCAGTTTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1624
OY 1806 CATGTATATATATATATATATATATATATATATATATATATATATATATATATAT 1851
Db 1625 AGTGTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1670

```

RESULT 11
 ABN95645
 ID ABN95645 standard; DNA; 1670 BP.

AC ABN95645;
 DT 13-AUG-2002 (first entry)
 DE Gene #2143 used to diagnose liver cancer.

KW Gene: liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cytostatic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.

OS Homo sapiens.

PN WO200229103-A2.

PD 11-APR-2002.

QY 556 GTCAAGAGCCAAAGAACTGCTGGCTGAAAGAGCAGTCTATGTGGCGTCTGGATCCAG 615
 DB 431 GTCAAGAGCCAAAGAACTGCTGGCTGAAAGAGTGTCTATGTGGCGTCTGGATCCAG 490
 QY 616 CCCCTCTCTGCTATACCTGACCTTCATCTTTGGCCAGCTGAGCCAGGAGGACATCAGTC 675
 DB 491 CCCCTCTCTGCTATACCTGACCTTCATCTTTGGCCAGC-----TCAGTG 535
 QY 676 AGGGGATGAGCAGTATACCTGACCTTCATCTTTGGCCAGCTGAGCGTGTGTGT 735
 DB 536 AGGCGATGAGCAGTATACCTGACCTTCATCTTTGGCCAGCTGAGCGTGTGTGT 595
 QY 736 TTCAATTCAGCATTAATGAGTGGGTCTCATCTCCGCGCATTCCTCTCTCTGT 795
 DB 596 TCCATTTTCAGCATTAATGAGTGGGTCTCATCTCCGCGCATTCCTCTCTCTGT 655
 QY 796 ACTGCATCATCTCTCTAAGCTGTACACTCCAGGCGCCAGGAGGCGCAAGGCCCTCA 855
 DB 856 ATTGCATTCATCTCTCAAGCTGTACACTCCAGGCGCCAGGAGGCGCAAGGCCCTCA 715
 QY 716 AGACACAGTATCTCTCAAGCTGTACACTCCAGGCGCCAGGAGGCGCAAGGCCCTCA 775
 DB 916 TCAGCATGAGCTCTCTCAAGCTGTACACTCCAGGCGCCAGGAGGCGCAAGGCCCTCA 975
 QY 776 TCAGCATGAGCTCTCTCAAGCTGTACACTCCAGGCGCCAGGAGGCGCAAGGCCCTCA 835
 QY 976 TTGTGCACAGTGTATCTCATCAGAGAGGCCCTCTCTCTCTCTCTCTCTCTCTCAAGC 1035
 DB 836 CTGTGCACAGTGTATCTCATCAGAGAGGCCCTCTCTCTCTCTCTCTCTCTCTCAAGC 895
 QY 1036 CCATCTCTATGCTCAAGC 1095
 DB 896 CCATCTCTATGCTCAAGC 955
 QY 1096 CCATGAGCAGAGGCTCAAGC 1155
 DB 956 CTGTGAGCAGAGGCTCAAGC 1015
 QY 1156 CCGTCTCCAGGAGTCAAGC 1215
 DB 1016 CTGTCTCCAGTGTATCTCATCAGAGAGGCCCTCTCTCTCTCTCTCTCTCTCTCTCAAGC 1067
 QY 1216 TAT 1275
 DB 1068 TAAAGACTTTTAT 1127
 QY 1276 AAGAGACTGACAGTCTGTACAGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1335
 DB 1128 AAAAGACTGACAGTCTGTACAGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1181
 QY 1336 GTTCTCTAGTCTGTGTAGAGTGTAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1395
 DB 1182 GTTCTCTAGTCTGTGTAGAGTGTAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1237
 QY 1396 CATGGAATGAGCGCTGAGGAGGAGCGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 1455
 DB 1238 CATATGATGTGTGTGTAGGAGGAGCGTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1297
 QY 1456 TGTAGACTGTGTAGAGTGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1515
 DB 1298 GGTAGACTGTAGAG-----AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1349
 QY 1516 ATAAGACTGAGCGGTATCTCTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1551
 DB 1350 GTAAGCTAGGAATGATCCCGCAGCTGTATATCATATA 1385

RESULT 14
 AAF20896
 ID AAF20896 standard; DNA; 5161 BP.

XX AAF20896;
 AC 14-MAR-2001 (first entry)
 DT Human CCR-4 CC chemokine receptor polynucleotide fragment #2463.
 DE
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antisthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 XX Homo sapiens.
 OS
 XX MO200062736-A2.
 PN
 XX 26-OCT-2000.
 PD
 XX 24-MAR-2000; 2000MO-US08020.
 PF
 XX 06-APR-1999; 99US-0127958.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 PI Nyce JW;
 XX
 DR WPI: 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 XX trigger adenosine receptors during metabolism, useful e.g. for treating
 XX cancers and respiratory obstructions -
 PS
 XX Disclosure: Page 290-291; 1592pp; English.
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antisthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, such as stimulating factors,
 CC immunoglobulins and antibodies, antibody receptors, transcription factors,
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention.
 CC
 CC Sequence 5161 BP; 1160 A; 1338 C; 1287 G; 1376 T; 0 other;

Query Match	49.8%;	Score 934;	DB 21;	Length 5161;
Best Local Similarity	81.6%;	Pred. No. 1e-166;		
Matches 1157;	Conservative 0;	Mismatches 220;	Indels 41;	Gaps 5;
QY	134	TGTGATATATACCTTCTGATCTGATGAGAGTGGGCTCGAGACTATGATC	193	
DB	3178	TTTGAGATATACCTTCTGATCTGATGAGAGTGGGCTCGAGACTATGATC	3237	
QY	194	CACAGAGAACCTCTCCGGATGAAAGCTCATTTGATAGATCTCTCCGAC	253	
DB	3238	CATGAGAGAACCTCTCTCCGGATGAAAGCTCATTTGATAGATCTCTCCGAC	3297	
QY	254	CATCTACTTATCATCTTCTGATGATGATGATGATGATGATGATGATGAT	313	
DB	3298	CATCTACTTATCATCTTCTGATGATGATGATGATGATGATGATGATGAT	3357	
QY	314	GGGTTACCAAGAAAGCTAGAGCATGACGACAAAGTACCGGCTGACCTTCAGTGC	373	
DB	3358	GGGTTACCAAGAAAGCTAGAGCATGACGACAAAGTACCGGCTGACCTTCAGTGC	3417	
QY	374	TGACCTCTCTTGTATCATCACTCCCTCTTGGGAGTTGATGATGATGATGAT	433	
DB	3418	CGACCTCTCTTGTATCATCACTCCCTCTTGGGAGTTGATGATGATGATGAT	3477	
QY	434	CTTTGGGAAATTTTGTATGAGGCTGTCCATATCATCTACACTGTCACCTTACAGCAG	493	
DB	3478	CTTTGGGAAATTTTGTATGAGGCTGTCCATATCATCTACACTGTCACCTTACAGCAG	3537	
QY	494	CGTTCTCATCTCTGCTTATCATGACCTGACCGGATGACCTGACCTGACCTGAC	553	
DB	3538	TGTCTCTCATCTCTGCTTATCATGACCTGACCGGATGACCTGACCTGACCTGAC	3597	
QY	554	CAGTCAAGGCGCAAGAAAGCTGCTGCTGAAAGAGCATCTATGAGGCTGATGCC	613	
DB	3598	CAGTCAAGGCGCAAGAAAGCTGCTGCTGAAAGAGCATCTATGAGGCTGATGCC	3657	
QY	614	AGCCCTCTCTGCTTATCATGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCT	673	
DB	3658	TGCCCTCTCTGCTTATCATGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCT	3702	
QY	674	TCAGGGGAGTACAGGTATCATGATGACCGCTTACCCCGATAGCCTGATGATGAT	733	
DB	3703	TCAGGGGAGTACAGGTATCATGATGACCGCTTACCCCGATAGCCTGATGATGAT	3762	
QY	734	CTTTCAATTCAGATATATGATGATGATGATGATGATGATGATGATGATGAT	793	
DB	3763	CTTTCAATTCAGATATATGATGATGATGATGATGATGATGATGATGATGAT	3822	
QY	794	TTACTGATCATCTCTGATGATGATGATGATGATGATGATGATGATGATGAT	853	
DB	3823	CTATTGATCATCTCTGATGATGATGATGATGATGATGATGATGATGATGAT	3882	
QY	854	CAGAGCATGATCTCTGATGATGATGATGATGATGATGATGATGATGATGAT	913	
DB	3883	CAGAGCATGATCTCTGATGATGATGATGATGATGATGATGATGATGATGAT	3942	
QY	914	GATCAGCATGATCTCTGATGATGATGATGATGATGATGATGATGATGATGAT	973	
DB	3943	GATCAGCATGATCTCTGATGATGATGATGATGATGATGATGATGATGATGAT	4002	
QY	974	CATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1033	
DB	4003	CATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	4062	
QY	1034	CCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1093	
DB	4063	CCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	4122	
QY	1094	CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1153	
DB	4123	CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	4182	
QY	1154	TTCCGTTCTCAGGAGTGAATCTCTCAGTTTCTCAGTTTCTCAGTTTCTCAGTT	1213	

DB	4183	ATCTGTTTCACATGATGATGATGATGATGATGATGATGATGATGATGATGAT	4234	
QY	1214	CTTAT	1273	
DB	4235	TGTAAAGACCTTTTATATATATATATATATATATATATATATATATATAT	4294	
QY	1274	ATAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1333	
DB	4295	ATAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	4348	
QY	1334	ATGTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1393	
DB	4349	GTTTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT	4404	
QY	1394	TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1453	
DB	4405	TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	4464	
QY	1454	TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1513	
DB	4465	GTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	4516	
QY	1514	GATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1551	
DB	4517	ACGTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	4554	
RESULT 15				
AAA34774	standard; DNA; 5161 BP.			
AAA34774	(first entry)			
28-JUL-2000	Human adenosine receptor related polynucleotide SEQ ID NO:2463.			
Human:	adenosine receptor; low adenosine antisense oligonucleotide;			
KW	phosphorothioate; impaired respiration; inflammation; allergy;			
KW	allergic disease; bronchoconstriction; inhibitor; antiinflammatory;			
KW	antiallergic; antischistosomal; cytoskeletal; analgesic; impaired airway;			
KW	lung disease; ischemic condition; pulmonary vasoconstriction; asthma;			
KW	respiratory distress syndrome; pain; cystic fibrosis; emphysema;			
KW	pulmonary hypertension; chronic obstructive pulmonary disease; COPD;			
KW	cancer; leukemia; lymphoma; carcinoma; metastasis; ss.			
OS	Homo sapiens.			
PN	WO200009525-A2.			
PD	24-FEB-2000.			
PF	03-AUG-1999; 99WO-US17712.			
PR	03-AUG-1998; 98US-0095212.			
PA	(UYEC-) UNIV EAST CAROLINA.			
PI	Nyce JW.			
DR	WPI; 2000-205971/18.			
PT	New antisense oligonucleotides useful for treating e.g. pulmonary			
PT	vasoconstriction, inflammation, allergies, asthma, hypertension,			
PT	bronchitis, emphysema, respiratory distress syndrome, ischemia or			
PT	cancers			
PS	Disclosure: Page 600-601; 1343pp; English.			
CC	The present invention describes a new composition comprising an			
CC	antisense oligonucleotide (ON) with low adenosine (up to 15%), which			
CC	targets nucleic acids involved in bronchoconstriction, allergies, and/or			

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OM nucleic - nucleic search, using sw model

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(without alignments)
7778.815 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/lna/Dackfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	974.4	51.9	1737	1	US-08-202-056-4
2	974.4	51.9	1737	1	US-08-076-093A-3
3	974.4	51.9	1737	1	US-08-701-265-3
4	974.4	51.9	1737	2	US-08-284-586-3
5	974.4	51.9	1737	2	US-08-805-478-3
6	974.4	51.9	1737	2	US-08-802-627A-3
7	974.4	51.9	1737	2	US-08-801-228-3
8	974.4	51.9	1737	2	US-08-801-228-3
9	974.4	51.9	1737	3	US-09-104-296-3
10	974.4	51.9	1737	3	PCT-US94-06380-2
11	952.8	50.8	1679	4	US-09-517-6205-14
12	951.8	50.7	1664	4	US-09-582-224A-5
13	834.6	44.5	1317	1	US-08-153-848-45
14	834.6	44.5	1317	3	US-09-299-843A-45
15	834.6	44.5	1317	3	US-09-088-337B-45
16	834.6	44.5	1317	5	PCT-US93-11153-45
17	198.4	10.6	1679	1	US-08-202-056-6
18	198.4	10.6	1679	1	US-08-076-093A-5
19	198.4	10.6	1679	1	US-08-701-265-5
20	198.4	10.6	1679	2	US-08-284-586-5
21	198.4	10.6	1679	2	US-08-805-478-5
22	198.4	10.6	1679	2	US-08-802-627A-5
23	198.4	10.6	1679	2	US-08-801-228-5
24	198.4	10.6	1679	2	US-08-801-228-5
25	198.4	10.6	1679	3	US-09-104-296-5
26	198.4	10.6	1679	3	PCT-US94-06380-3
27	198.4	10.6	2818	3	US-08-982-493-7

28	198.4	10.6	2818	4	US-08-628-655-1	Sequence 1, Appl
29	195.8	10.4	2085	3	US-09-299-843A-65	Sequence 65, Appl
30	195.8	10.4	2085	4	US-09-088-337B-65	Sequence 65, Appl
31	193.8	10.3	1670	3	US-08-709-838-1	Sequence 1, Appl
32	193.8	10.3	1670	4	US-08-829-838-1	Sequence 1, Appl
33	186.8	10.0	2751	1	US-08-153-848-23	Sequence 23, Appl
34	186.8	10.0	2751	4	US-09-299-843A-23	Sequence 23, Appl
35	186.8	10.0	2751	4	US-09-088-337B-23	Sequence 23, Appl
36	186.8	10.0	2751	4	PCT-US93-11153-23	Sequence 23, Appl
37	183.8	9.8	1373	5	PCT-US92-02977-6	Sequence 6, Appl
38	183.8	9.8	1373	5	PCT-US95-03032-3	Sequence 3, Appl
39	182	9.7	1900	1	US-08-153-848-18	Sequence 18, Appl
40	182	9.7	1900	4	US-09-299-843A-18	Sequence 18, Appl
41	182	9.7	1900	4	US-09-088-337B-18	Sequence 18, Appl
42	182	9.7	1900	5	PCT-US93-11153-18	Sequence 18, Appl
43	182	9.7	2058	1	US-08-153-848-6	Sequence 6, Appl
44	182	9.7	2058	3	US-09-299-843A-6	Sequence 6, Appl
45	182	9.7	2058	4	US-09-088-337B-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-202-056-4
; Sequence 4, Application US/08202056
; Patent No. 5440021
GENERAL INFORMATION:
; APPLICANT: Chuntarapat, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (genentech)
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,056
; FILING DATE: 25-FEB-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P3
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5350
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 bases
; TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-202-056-4
Query Match 51.9%; Score 974.4; DB 1; Length 1737;
Best Local Similarity 76.1%; Pred. No. 2.1e-187;
Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

QY	50	CCAGGTACCACTGAGACCCCTCGTAGGGGCTTTGGTGGCTCCGGGTACACCAACCGGCTGTAGAGC	109
Db	20	GCGCCGCGCAAAAGTAGACGCCCGAAGGGCCCTGAGTGGCTCCAGTGAAGCCACCGCATCTTGGAGAAC	79
QY	110	GAGTGTTCCTCCATGNAACCGATCAGTGTGAGATATACACTTCTGTATTACTACTCTGTGAAGA	169
Db	80	CAGCGGTTAACCATGGA-----GGGGATCAGTATATATACCTTCAGATTAACCTACACCGAGAGA	134
QY	170	AGTGGGGTCTGGAGACTTGTACTCCACAGAAGAACCTGCTTCCGGGTGTAAGAGTCCA	229
Db	135	AATGGGCTCAGAGGGACTATGACTCCATGAAAGAACCCGTTCCGTGTAAGAAATGTCTAA	194
QY	230	TTTCAATGGAATCTTCCTGGCCACCATGTACTGTATCATCTCTTGTGATGGCATATGTGG	289
Db	195	TTTCAATTAATTTCTTCTGTCGCCACCATTACTCCATCATCTTCTTAAGTGGCATTTGGG	254
QY	290	CAATGAGATTGGTGAATCCTGTATGAGGTATTACAGAAAGAGCTGAAGSACATAGAGSACAA	349
Db	255	CAATGAGATTGGTGAATCCTGTATGAGGTATTACAGAAAGAACTGAAAGACATAGAGSACAA	314
QY	350	GTACCGGCTGCACTGTGATGAGGCTGACCTCCTCTTGTATCATCACTCCCTCTTGTGGC	409
Db	315	GTACAGGCTGCACTGTGATGAGGCGACCTCTCTTGTATCAACGCTCCCTCTGTGGC	374
QY	410	AGTTGATGCCAATGGCTGATGCTGATGAGTATTGGGAAATTTTGTGTAAAGGTGTGCATATCAT	469
Db	375	AGTTGATGCCGCTGGGAAATCGTATCTTGGGAACTCTATGCAAGAGGATGATGTAT	434
QY	470	CTACACTGTCAACCTCTACAGCAGCGTCTCATCCTGTGCCTTCATCAGCCTGAGACGGTA	529
Db	435	CTACAGCATCAACCTCTACAGCAGTGTCTATCTGTGCCCTTCATCAGTCTGGACGGTA	494
QY	530	CTGTGCCATTTGTCCAGCGCCACCAACAGTCAAAAGGCCAAGAAACTGTGTGTAAGAAAGC	589
Db	495	CCTGGCCATCTCTCCAGCGCCACCAACAGTCAAGAGGCCAAGAAAGCTGTGGCTGAAGAAAGT	554
QY	590	AGCTATATGTGGGCGTGGATGCCAGCGCCCTCTCTGTACTATTAAGTACTGACTTCACTTTGGC	649
Db	555	GGTCTATATTTGGCGTGTGGATGCCCGCCCTCTCTGTGACTATTTCCCGACTTCACTTTTGGC	614
QY	650	CGAGCTCAGCCAGAGGGGAGCATAGTCAAGAGGGGATGACAGGTACATCTGTGACCGGCTTTTA	709
Db	615	CAAGC-----TCAGTGAAGGACAGATGACAGATATATCTGTGACCGGCTTTA	659
QY	710	CCCCGATAGCCTGTGAGATGTGTGTGTTTCAATTCACAGATATATGTGTGGTCTTCATCTT	769
Db	660	CCCCATACATTTGTGGTGTGTGTGTGTTCACATTTTCAGACATCATAGTGTGGCCTTATCTT	719
QY	770	GGCGGGATGCTCATCTCTCTGTATCTAGATCATCATCTCTAAGCTGTGCACACTCCAA	829
Db	720	GGCTGTGATTTCTATCTCTCTCTGTATTTGATATATCTCTCTCAAGGCTGTACACTCCAA	779
QY	830	GGGCGACAGAGCGCAGAGGCCCTCAAGACAGCATGTCTCATCTCAAGCTTCTTTTGGC	889
Db	780	GGGCGACAGAGCGCAGAGGCCCTCAAGACAGCATGTCTCATCTCTCTCTTCTTCTTGGC	839
QY	890	CTGCTGCTGCATATTTATGTGGGATCAGCATGACATCTTTCATCTCTTTTGGAGTCAAT	949
Db	840	CTGTGTGGCTGTACTACTATTTGGGATCAGATGACATCTTTCATCTCTTCTTGGAGTCAAT	899
QY	950	CAAGCAGAGGATGTACTTTCAGAGACATTTGTGCACATGTGATCTTCATCAGAGAGCCCT	1009
Db	900	CAAGCAGAGGATGTACTTTCAGAGACATGTGATGATGATTTTCATCAGAGAGCCCT	959
QY	1010	GGCCTTCTTCACATGTTGCGCGAAGCCCATCTCATGATCCCTTCGCGGGGCGCAAGTCA	1069
Db	960	AGCTTTCTTCACATGTTGCTGAAACCCCATCTCTATGCTTCTCTTGGAGCGCAATTTAA	1019
QY	1070	AAGCTCTGCCAGCATGACTCAATCTCATAGAGAGAGGCTCCAGAGCTCAAGATCTTTTC	1129
Db	1020	AAGCTCTGCCAGCATGACTCAATCTCATAGAGAGGCTCCAGAGCTCAAGATCTCTTTC	1079
QY	1130	CAAAAGAAAGCGGGGTGACACTCTTCCGCTCCACGGAATGCAGATCTCTCAACTTTTCA	1189

[illegible]

Db 1582 -----TTTTTCAGTTTTCAGAGAGTGGGTGATTTTCAGCACTAC-AGT 1623

QY 1790 GTACAGCTCTGTTATCTATCTGTTAATAAGTCATGAACCTTAAAAA 1849

Db 1624 GTACAGCTCTGTTATCTGTTAATAAGTCATGAACCTTAAAAA 1683

QY 1850 AAAAAAAAAAAAAAAAAAAAAA 1877

Db 1684 AAAAAAAAAAAAAAAAAAAAAA 1711

RESULT 3

US-08-701-265-3

Sequence 3, Application US/08701265
Patent No. 5776457

GENERAL INFORMATION:

APPLICANT: Chuntharapat, Anan

APPLICANT: Lee, James

APPLICANT: Hebert, Caroline

APPLICANT: Jin Kim, K.

TITLE OF INVENTION: Antibodies to Human PFA4 Receptors

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/701,265

FILING DATE: 22-AUG-1996

CLASSIFICATION: 424

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/076093

FILING DATE: 11-Jun-1993

APPLICATION NUMBER: 07/810782

FILING DATE: 19-DEC-1991

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 07/677211

FILING DATE: 29-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: 706P2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1737 nucleotides

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

US-08-701-265-3

Query Match 51.9%; Score 974.4; DB 1; Length 1737;

Best local Similarity 76.1%; Pred. No 2,1e-187;

Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

QY 50 GCAGGTAGAGTACCTCTGAGGCGTTGGTCTCCGTAACCAACGAGCTGTAGAC 109

Db 20 GCGGCGCGAAGTGAAGCGCGGCGCTGAGTCTCAGTAGACGAGCTGTAGAC 79

QY 110 GAGGTGTCATGAGCAACCATCATGAGTGTGATATATACCTTCTGATTAACCTACTCTGAGA 169

Db 80 CAGCGGTACCATGGA-----GGGATCAGATATATACCTTCTGATTAACCTACTCTGAGA 134

QY 170 AGTGGGCTGTGAGAGATATGACTCCACAGGAGACCTCTCCGGATGAAGCTCCA 229

Db 135 AATGGGCTGAGGAGATATGACTCCACAGGAGACCTCTCCGGATGAAGAGTCA 194

QY 230 TTTCAATAGGATCTTCTGCGCCAGCATCTTCTGATGAGTGTAGTGG 289

Db 195 TTTCAATAGGATCTTCTGCGCCAGCATCTTCTGATGAGTGTAGTGG 254

QY 290 CAATGATGATGATCTTCTGCGCCAGCATCTTCTGATGAGTGTAGTGG 349

Db 255 CAATGATGATGATCTTCTGCGCCAGCATCTTCTGATGAGTGTAGTGG 314

QY 350 GTACCGGCTGACACCTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 409

Db 315 GTACCGGCTGACACCTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 374

QY 410 AGTTGATGATGATCTTCTGCGCCAGCATCTTCTGATGAGTGTAGTGG 469

Db 375 AGTTGATGATGATCTTCTGCGCCAGCATCTTCTGATGAGTGTAGTGG 434

QY 470 CTACAGTGTACACCTCTGAGAGGCTTCTGATGAGTGTAGTGGTGGTGG 529

Db 435 CTACAGTGTACACCTCTGAGAGGCTTCTGATGAGTGTAGTGGTGGTGG 494

QY 530 CCGGCGCATGTCACAGGCGCCAGCATCTTCTGATGAGTGTAGTGGTGG 589

Db 495 CCGGCGCATGTCACAGGCGCCAGCATCTTCTGATGAGTGTAGTGGTGG 554

QY 590 AGTCTATGATGATGATCTTCTGCGCCAGCATCTTCTGATGAGTGTAGTGG 649

Db 555 AGTCTATGATGATGATCTTCTGCGCCAGCATCTTCTGATGAGTGTAGTGG 614

QY 650 CGACGTGACAGGAGGAGATGATGAGTGTAGTGGTGGTGGTGGTGGTGG 709

Db 615 CGACGTGACAGGAGGAGATGATGAGTGTAGTGGTGGTGGTGGTGGTGG 669

QY 710 CCGGCGCATGTCACAGGCGCCAGCATCTTCTGATGAGTGTAGTGGTGG 769

Db 660 CCGGCGCATGTCACAGGCGCCAGCATCTTCTGATGAGTGTAGTGGTGG 719

QY 770 GCGGCGCATGTCACAGGCGCCAGCATCTTCTGATGAGTGTAGTGGTGG 829

Db 720 GCGGCGCATGTCACAGGCGCCAGCATCTTCTGATGAGTGTAGTGGTGG 779

QY 830 GCGGCGCATGTCACAGGCGCCAGCATCTTCTGATGAGTGTAGTGGTGG 889

Db 780 GCGGCGCATGTCACAGGCGCCAGCATCTTCTGATGAGTGTAGTGGTGG 839

QY 890 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 949

Db 840 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 899

QY 950 CAAGCAAGGATGTGATGATGATGATGATGATGATGATGATGATGATGAT 1009

Db 900 CAAGCAAGGATGTGATGATGATGATGATGATGATGATGATGATGATGAT 959

QY 1010 CCGGCGCATGTCACAGGCGCCAGCATCTTCTGATGAGTGTAGTGGTGG 1069

Db 960 CCGGCGCATGTCACAGGCGCCAGCATCTTCTGATGAGTGTAGTGGTGG 1019

QY 1070 AAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1129

Db 1020 AAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1079

QY 1130 CAAGCAAGGATGTGATGATGATGATGATGATGATGATGATGATGATGAT 1189

Db 1080 CAAGCAAGGATGTGATGATGATGATGATGATGATGATGATGATGATGAT 1139

QY 1190 CTGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1249

Db 1140 CTGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1199

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OY      1250 TTTTATGTCACACTTTTCCAGATATAAGACAGCAGCTGTGTACAGTTTTTTTTT
Dd      1192 TTTTAAGTACACAATTTCACGATATAAAGACTGACCATAATTGTACGTTTTATTGCC
OY      1310 TTTTAAATGGACGTGGAGCTTAATGTTCCCTAGTTTTTGAGAGTTTACTTAATTT
Db      1252 TTGTTGGATTTTGTCT-----CTTGTTGTTCTTAGTTTTTGTGAAGTTTAATGACTTA
OY      1370 ATATAAATATTGTTTTTTGTTGTTTCACTGTGAATGAGCGCTGACGACACTGTGGCC
Db      1306 TTTTATA----TAAATTTTTTTTGTTCATATGTAATGTGTGCTGAGGCAGCCTGTGGCC
OY      1430 AAGTCTTAGTAGCGTTTATCTGNGTBTAGACGCTGAAGCTGTAGAAGGAAGAAACGTA
Db      1362 AAGTTCTTAGTGTGCTGTAATGTCTGTGGTAGAGACTGTAGA-----AAGGGAACTGA
OY      1490 ACATTCCAGAAATGtGTGTAATTAATGAATAAAGCTAGCCGTANFCTCACGCTGTGTCGA
Db      1414 ACATTCCAGACCGTGTAGTAATCATCCGTAANAAGCTAGAAATGATCCCCAGCTGTTATGCA
Db      1550 TAATCTCTCAATTCGAGAGACACCCCACCCCCACCCCCACCCCATTTCTTAAT
Db      1474 TAGATAATCTCTCCA-----
OY      1610 TGTTGGTATGCTGCTGTGATGAGTGTGTTGTTGTTTTTTTGTGTGTGTTGTTTTT
Db      1489 -----TTCCCGTGAACGTTTTCCTGTTCTTAAGACGTAT
OY      1670 TTTTCTGTAAAGATGACACTTAACCAAAGCCGAAATGSGTGTAGAAATGCTGGGGT
Db      1526 TTTCGTGTAGAGATGGCAGCTTAATACCAAGCCCAAGGTGT-ATAGAAAATGCTGG--
OY      1730 TTTTTTTGTTGTTGTTTTTTCAGATTTTCAAGAGTGAATGTGACTTTCAGTCCATCAAT
Db      1582 -----TTTTTCAGTTTTCAGAGAGTGGGTGATTTCAGCACTTAC-Agt
OY      1790 GTACAGTCTGTATTACTTGTATTATAAAGTCAATGATTAACCTTAATAAAAAAAAAAAAA
Db      1624 GTACAGCTCTGTATTAACTGTATTATAAAGTACATGTTAAACTTAATAAAAAAAAAAAAA
OY      1850 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1877
Db      1684 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1711

RESULT 4
US-08-284-586-3
Sequence 3, Application US/08284586
Cent No. 5840856
GENERAL INFORMATION:
APPLICANT: Chuncharapal, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: jin kim, K.
TITLE OF INVENTION: Antibodies to Human Pf4 Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284_586
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

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? APPLICATION NUMBER: US/08/076,093A
 ? FILING DATE: 11-Jun-1993
 ? APPLICATION NUMBER: 07/810782
 ? FILING DATE: 19-DEC-1991
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 07/677211
 ? FILING DATE: 29-MAR-1991
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Love, Richard B
 ? REGISTRATION NUMBER: 34,659
 ? REFERENCE/DOCKET NUMBER: 706P2
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 415/225-5530
 ? TELEFAX: 415/952-9881
 ? TELE: 910/371-7168
 ? INFORMATION FOR SEQ ID NO: 3:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 1737 nucleotides
 ? TYPE: Nucleic Acid
 ? STRANDEDNESS: Single
 ? TOPOLOGY: Linear
 US-08-284-586-3

Query Match	51.9%;	Score 974.4;	DB 2;	Length 1737;
Best Local Similarity	76.1%;	Pred. No. 2.1e-187;		
Matches 1391;	Conservative	0;	Mismatches 301;	Indels 136; Gaps 10

QY 50 GCAGGTAGACGAGACCCTTGGAGGGCGTTTGAGTCCTCCGGTAACCAACGCGCGTGTGAGC 109

Dd 20 GCGCGGCCGAANGTAGACCCCGGAGGGCGCTAGTGCTCTCAAGTACGCACCGCATCTGGAGAAC 79

QY 110 GAGTGTGGCCATNGAAGCACCGATCAGTGTGATATATACACTTCTGATMACTACTCTGAAGA 169

Dd 80 CAGCGGTATACCATGGA-----GGGGATCAGTATATACACTTCTGATMACTACTACACCGAGA 134

QY 170 AGTGGGGTCTGGAGACTATGACTCCACAACAAGAACCTCTGCTCCGGGATGAACACTCCA 229

Dd 135 AATGGGCTCAGGGGACTATGACTCATGAAAGAACCTCTTCCGGAAGAAAATCTTA 194

QY 230 TTTCATATGAGATCTTCCTCCACCACATCTACATTTCATCTTCTTACAGGCGATAGCGG 289

Dd 135 TTTCAATAAATCTTCTCTCCACCACATCTACATCATCTTCTTAACTBGCATTGTGGC 254

QY 280 CAATGGATTGTATCTGTGTCATGGGTTACCAAGAAGACGTAAGGAGCATGACGACAA 349

Dd 255 CAATGGATTGTATCTGTGTCATGGGTTACCAAGAAGAACGTAAGGAGCATGACGACAA 314

QY 350 GTACCGGGCTGCACCTGTCAAGTGGCTACCTCCTCTTTGTATATACACTCCCCTTTGCGC 409

Dd 315 GTACAGGGCTGCACCTGTCAAGTGGCGACCTCCTCTTTGTATATACACTCCCCTTTGCGC 374

QY 410 AGTTATGTCATGCGCGATGCTGTACTTTGGGAAATTTTGTGTAAGGCGTGCATATCAT 469

Dd 375 AGTTATGCGCGTGGCGAAGCTGTACTTTGGGAATCTCTATGCAAGGCACTCATGTCTAT 434

QY 470 CTACACTGTCAACCTCTACAGACGCGTTCTCATCTCGGCGCTTCATCAGCGCTGACCGGTA 529

Dd 435 CTACACAGTCACACTCTACAGACGTTCTCATCTCGGCGCTTCATCAGTCGTGACCGGTA 494

QY 530 CCTGCCCATTTGTCCACGCGCACCAAGTAAAGGCGCAAGGAACCTGTGCTAAAAAGC 589

Dd 485 CCTGGCCATCTGTCCACGCGCACCAAGTCAAGAGGCGCAAGGAACCTTTGGCTAAAAAGT 554

QY 590 AGTATATGAGGCGTGTGATCCCAAGCCCTCTCCCTGACATATACCGAGCTTCATCTTTGC 649

Dd 555 GGTCTATGTGGCGTGTGATCCCTGCTCCTCTGCTGACTATTCCTCGACTTCATCTTTGC 614

QY 650 CGAGCTACGCCAAGGGGGAATCAGTCAAGGAGGATGACAGTATCATCTGTACCGCGCTTTA 709

Dd 615 CAACG-----TCAGTAGGCGACAGTACAGATATATCTGTGAGCGCTTCNA 659

QY 710 CCCCATATCCCTGTGATGTGTGTTCATATTCACGCAATATATAGTGGGTCTCATCTCT 769

Db	660	CCCCAATGACTTGGGGGCGTGGTGGTCCAGTTTCAGACATTCANAGGTTGGCCCTTATCCT	719
Qy	770	GGCCGGGCACTGTCATCCTCTCCTGTTACTGCATATCATCTCTAAGCTGTACACTCCAA	829
Db	720	GCCTGGTATTTTCTACCTCCTGCTCCTATATGATTATATCTCCAGAGTGTACACTCCAA	779
Qy	830	GGGCGCCAGAGAAGGCAAGGCCCTCAAGACAGACATGCTCCTCAATCCAGTTTCTTTGCG	889
Db	780	GGCGCCACGAGAAGGCGCAGAGGCCCTCAGAACCCACAGTCACTCATCCTCGGCTTCTTCGC	839
Qy	890	CTGCTGCTGCCATATTATATGTTGGGAGTACAGCATGCATCTCTTCATTCCTTTTGGAGTCAT	949
Db	840	CTGTTGGCTGCTTACTACTCATTTGGGATTCAGATGCAGACTCTTCATATCCCTCGGAATCAT	899
Qy	950	CAGCAAGAGATGTGACTTCGAGAGCATGTGTCACAAAGGAGTATCCATCAAGAGGGCCT	1009
Db	900	CAGCAAGAGGTTGTAGTTTGAGAACACTGTGCACAAAGTGGATTTTCATCACCGAGCCCT	959
Qy	1010	CGCCTTCTTCACATGTTGCCCTGAACCCCATCCCTATGCTCTCCTCGGGGGCAAGTTTCAA	1069
Db	960	AGCTTTTCTTCACATGTTGTGTGAACCCCATCCTCATGCTCTTCCCTGGAGCAAAATTAA	1019
Qy	1070	AAGCTCTGCCAGATGTCATCACTCACTCATGATGAGAGAGGCTCCAGCCCTCAAGATCCTTTC	1129
Db	1020	AACCTGTGCCAGCACGCACTCCTCTGTGAGAGAGGTCACAGCCTCAAGATCCTCTC	1079
Qy	1130	CAAAAGGAAGCGGGGTGGACACTCTTCCGTCTCCACGAGAGTCACAATCCTCAAGTTTCA	1189
Db	1080	CAAGGAAGGAGAGGTGACATTCATCTTTCCACTAGCTGAGCTTCACAGTTTCA	1139
Qy	1190	CTCCAGCTAACCCCTTATGCAAAAGCTTATATAATATATATATATATGATTAAGAACTT	1249
Db	1140	CTCCAGCTTAA-----CACAGATGTAAGAAAGACTTTTTTTTAAATATGATTAATAGCTTTT	1191
Qy	1250	TTTATATGTACACATTTTCCAGATATAGAGACTGACAGCTGTGTACAGTTTATTTT	1309
Db	1192	TTTTATAGTTACACATTTTTCAGATATATAAAGACTGACCAATATGTGACGTTTATTGCG	1251
Qy	1310	TTTTTAAATGACCTGTGGAGTTATATGTTCTCTAGATTTTTGTGAGGTTTGACTTAATTT	1369
Db	1252	TTGTGTGAGTTTTTGT-----CTGTGTGTTCTTTAGTTTGTGAAGTTTAAATGACTTA	1305
Qy	1370	ATATATAATATGTTTTTTGTTGTTTCAATGAAAGACCGTCTGGGAGGACCGTGGCC	1429
Db	1306	TTTTATA-----TAATTTTTTTTTTTTGTTCATATGATGTGTCTTGGCAGGACCTGTGGCC	1361
Qy	1430	AAGTCTTAGTAGCTGTTATCTATCTGTGTAGAGCTGTAGAACTGTAGAGGAAGAACTGA	1489
Db	1362	AAGTCTTAGTAGCTGATGTGTGTGTGTAGAGACTGTGA-----AAGGAACTGA	1413
Qy	1490	ACATTTCCAGATGTGTGTAAATTTGAATAAGCTAGCCGTATCTCAAGCTGTGTGTGCA	1549
Db	1414	ACATTTCCAGACGCTGTAGTGAATATACGTAAAGCTAGAAATATATCCCAAGCTGTTTATGCA	1473
Qy	1550	TAAATCTCTTCAATTCGAGAGACACCCCAACCCCAACCCCAACCCCACTTCTTAAT	1609
Db	1474	TAGATTAATCTCTCCA-----	1488
Qy	1610	TGTTTGGTTATGCTGTGTGATGAGTTTGTGTGGTTTTTTTTTGTGTGTGTGTGTGT	1669
Db	1489	-----TTCCCGTGAAGAGTTTTCCTGTGTTCTTAAGACGTGAT	1525
Qy	1670	TTTTCTGTAAGATGCGCATTAAGCAAAAGCCGAAATGCTGTGAAATGCTGGGGT	1729
Db	1526	TTTGTGTAGAGATGCGCATTTATACCAAGGCCCAAGTGTGT-ATAGAAATGCTGTG---	1581
Qy	1730	TTTTTTTGTGTTGTGTTTTCAGTTTCAAGAGTATGTTGACTGTAGTCCCTAACAAAT	1789
Db	1582	-----TTTTTTCAGTTTTCAGAGGTGGTGTGATTTTCAGCACTTAC-AGT	1623
Qy	1790	GTACAGCTTGTATTTACTATGTTTATAAAGTCAATGATTAACCTTAAGAAAAA	1849
Db	1624	GTACAGCTTGTATTTAAGTGTGTATATAAAGTCAATGTTTAAAGTAAAAA	1683

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0Y 1850 AAAAAAAAAAAAAAAAAAAAAAAAAA 1877
Db 1684 AAAAAAAAAAAAAAAAAAAAAAAAAA 1711

RESULT 5
US-08-805-478-3
; Sequence 3, Application US/08805478
; Patent No. 5874543
; GENERAL INFORMATION:
; APPLICANT: Chuncharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: ANTIBODIES TO PRAA RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,478
; FILING DATE: 25-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706p2P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-805-478-3

Query Match 51.9%; Score 974.4; DB 2; Length 1737;
Best Local Similarity 76.1%; Pred. Mismatches 187;
Matches 191; Conservative 0; Indels 136; Gaps 10

0Y 50 GCAGGTACACGAGACCTCTGTGAGCGGTTGGCTCCGCTACACACCGCTGTAGAC 109
Db 20 GCGCGCGCCGAAGTACCGCCGAGGCGCTGAGTCTCAGTACCCACCGCATCTGGAGAC 79

0Y 110 GAGTGTGCCATGAGAACCGATCAGTGTGAGTATATACACTTCTGATTAACCTCTGAGAG 169
Db 80 CAGCGGTATACATGGA-----GGGATCAGTATATACACTTCAGATTAACCTACCGAGGA 134

0Y 170 AGTGGGCTCTGAGACACTATGATCCACAAGAACCCCTGCTCCGGGAGTGAAGAACCTCA 229
Db 135 AATGGGCTCAGGCGACTATGATCTCATGAGGAAGAACCTGTTCCGTGGAAGAAATGCTTA 194

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OY      230 TTTCAATAGATCTTCTGCGCACCATCTTATCATCTCTTGACGTGGCATAGTGG 289
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Db      195 TTTCAATAAATCTCTTCCGACCATCTCTCATCATCTCTTAATGAGTATGGG 254
OY      290 CAATGATGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 349
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      255 CAATGATGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 314
OY      350 GTACGGCTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 409
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      315 GTACAGGCTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 374
OY      410 AGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 469
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      375 AGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 434
OY      470 CTACACTGTCAACCTTACAGACAGCTTCTATCTGATGATGATGATGATGATGATG 529
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      435 CTACACAGTCAACCTTACAGACAGCTTCTATCTGATGATGATGATGATGATGATG 494
OY      530 CTTGCGCATGTTGACAGCCACCAACAGTCAAAAGCCAAAGAACTGCTGCTGAAAAGC 589
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      495 CTTGCGCATGTTGACAGCCACCAACAGTCAAAAGCCAAAGAACTGCTGCTGAAAAGC 554
OY      590 AGTCTATGTTGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 649
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      555 GGTATGATGTTGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 614
OY      650 CGAGCTGAGCCAGGGGGGACATCACTGAGGGGGATGACAGTACATCTGTGACCCCTTTA 709
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      615 CAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 659
OY      710 CCCGATAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 769
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      660 CCCGATAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 719
OY      770 GCCCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 829
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      720 GCCCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 779
OY      830 GGGCGACCAAGAGCGACAGGCGCTCAAGACAGATGATGATGATGATGATGATGATG 889
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      780 GGGCGACCAAGAGCGACAGGCGCTCAAGACAGATGATGATGATGATGATGATGATG 839
OY      890 CTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 949
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      840 CTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 899
OY      950 CAAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1009
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Db      900 CAAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 959
OY      1010 CGGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1069
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Db      960 AGTTTCTTCCACTGTTGCTGAACCCCATCTCTATGCTTCTCTGAGGCAATTTAA 1019
OY      1070 AAGCTCTGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1129
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1020 AAGCTCTGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1079
OY      1130 CAAGGAAAGGGGGGTGACACTCTCTCGTCCAGAGAGCAAAATCTCCAGTTTCA 1189
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Db      1080 CAAGGAAAGGGGGGTGACACTCTCTCGTCCAGAGAGCAAAATCTCCAGTTTCA 1139
OY      1190 CTCCAGCTAACCTTATGCAAAAGCTATATATATATATATATATATATATATATAT 1249
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1140 CTCCAGCTAACCTTATGCAAAAGCTATATATATATATATATATATATATATATAT 1191
OY      1250 TTTTATGTTACATTTTCCAGATATAGAGACTGACAGCTGTGACAGTTTCTTTT 1309
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1192 TTTTATGTTACATTTTCCAGATATAGAGACTGACAGCTGTGACAGTTTCTTTT 1251

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OY      1310 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1369
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1252 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1305
OY      1370 ATATATATATGTTTGTGTTTGTTCATGATGATGATGATGATGATGATGATGATG 1429
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1306 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1361
OY      1430 AAGTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1489
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1362 AAGTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1413
OY      1490 ACATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1549
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1414 ACATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1473
OY      1550 TAATCTCTTCAATTCAGAGAGACCCACCCACCCACCCACCCACCCACCTTAAAT 1609
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1474 TAGATATATCTCTCA-----TTCCGTTGGAAGCTTTTCTTAAAGCTGAT 1488
OY      1610 TGTGTTGTTATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1669
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1489 -----TTCCGTTGGAAGCTTTTCTTAAAGCTGAT 1525
OY      1670 TTTTCTGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1729
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1526 TTTCTGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1581
OY      1730 TTTTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 1789
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1582 -----TTTTCAGTTTTCAGAGTGGTGTGATTTTCAGCACCTAC-AGT 1623
OY      1790 GTACAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1849
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1624 GTACAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1683
OY      1850 AAAAAAAAAAAAAAAAAAAAAAAAAA 1877
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1684 AAAAAAAAAAAAAAAAAAAAAAAAAA 1711

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RESULT 6
US-08-802-627A-3
: Sequence 3, Application US/08802627A
: Patent No. 5892017
: GENERAL INFORMATION:
: APPLICANT: Lee, James
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: NUCLEIC ACID ENCODING P4A RECEPTOR
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/802,627A
: FILING DATE: 19-Feb-1997
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/284586
: FILING DATE: 10-Aug-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/076093
: FILING DATE: 11-Jun-1993
: PRIOR APPLICATION DATA:

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RESULT 7
US-08-801-238-3
; Sequence 3, Application US/08801238
; Patent No. 591896
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PFAA RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,238
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
08-801-238-3

Query Match          51.9%; Score 974.4; DB 2; Length 1737;
Best Local Similarity 76.1%; Pred. No. 2.1e-187;
Matches 191; Conservative 0; Mismatches 301; Indels 136; Gaps 10

QY 50 GCAGGTACAGTAGACCTCTGTAGAGCGTTGGTCTCCGTAACCAACCAAGCGCTGTAGAGC 109
   || || || || || || || || || || || || || || || || || || || || || ||
Db 20 GCGCGCGCGCAAGTAGACGCCCGACGSGCCCTGAGTGTCCAGTAGACCAACCGCATCTGAGAAC 79
   || || || || || || || || || || || || || || || || || || || || || ||
QY 110 GAGTGTCCCATGGAACCGATCAGTGTGAGTATATACACTTGTGATTAACCTACTCTGAAGA 169
   || || || || || || || || || || || || || || || || || || || || || ||
Db 80 CAGCGGTATACATGGA-----GGGGATCAGTATATACACTTCAGTAACTACACCGAGGA 134
   || || || || || || || || || || || || || || || || || || || || || ||
QY 170 AGTGGGCTGTGAGACTATGACTCCACAAGGAACCGCTCCGGGATMGAAAGCAAGCTCCA 229
   || || || || || || || || || || || || || || || || || || || || || ||
Db 135 AATGGGCTCAGGGGACTATGACTCATATAGGAACCGCTGTTTCCGTGAAGAAATGCTAA 194
   || || || || || || || || || || || || || || || || || || || || || ||
QY 230 TTTCATATAGACTTCTCTGCGCCACCATCTACTTTCATCTCTTCTGACTGGCATAGTCGG 289
   || || || || || || || || || || || || || || || || || || || || || ||
Db 195 TTTCATATAAATCTTCTGCGCCACCATCTACTTCATCTCTTAACTGGCATGTGTGG 254
   || || || || || || || || || || || || || || || || || || || || || ||
QY 290 CAATGATTTGGTATCTGTGTCATGGGTTACCAAGAAAGCTTAAGAGACTATGACGAGCA 349
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Db	255	CAATGGATTGGTATCCTGGTCATGGGTTACAGAAAGAACTGGAAGCATGACGGACAA	314
OY	350	GTACCGGCTGACCTGTGCAGTGGCTGACCTCTCTTTGTATACACTCCCTCTTG6GC	409
Db	315	TT	374
OY	410	AGTTGATGCCATGGCTGACTGGTACTTTGGGAAATTTTGGTAAGGCTGTCCATATCAT	469
Db	375	AGTTGATGCCGTGGCAACTGGTACTTTGGGAACTTCTATGCAAGGCAAGTCATGTCAAT	434
OY	470	CTACACTGTAAACCTCTACAGACAGCCCTTTCATCTCTGGCCCTTCATCAGCCTGACCGCTA	529
Db	435	CTACACAGTCAACCTCTACACAGACTGTCTCATCTCTGCTTCACTAGTCTGACCGCTA	494
OY	530	CTTCGCCATTGTCCAGCCACACCACTGACAAAGGCCAAGGAAACTGCTGGCTGAAAGGC	589
Db	495	CTTGCCCATGTCTCCAGCCACACCACTGACAGAGGCCAAGGAAAGCTGTGGCTGAAAGGT	554
OY	590	AGTTATGTGGGGCTGTGGATCCAGGCCCTCTCTGACTATACCTGACTTTCATCTTTGC	649
Db	555	GGTTATGTGGGGCTGTGGATCCCTGGCCCTCTGCTGACTATATCCCACTTCATCTTTGC	614
OY	650	CGAGCTGACGCCAGGGGGACATCACTGACGGGGATGACAGGTACTGTGTGACCCCTTTTA	709
Db	615	CACG-----TCACTGAGGACGATGACAGATATATCTGTGACCCCTTCTA	659
OY	710	CCCCGATAGCCTGTGGATGGTGGTGTTCATTTCCACCATATAAATGGTGGCTCATCTCT	769
Db	660	CCCCATGACTGTGGGGTGTGTGTTCACATTTCCACACATCATATGGTGGCTTATCTCT	719
OY	770	GCCCCGATGCTATCTCTCTCTTTACTGCTATATCTCTTAAGCTGTACACTCCAA	829
Db	720	GCCGTGATGTGATCCCTGCTCTCTATTGCTATTATCATCTCCAAAGCTGTCCACTCCAA	779
OY	830	GGGCTACAGAAAGGGCAAGGCCCTCAAGACAGACAGTATCCTCATCTAGTCTTTCTTGC	889
Db	780	GGGCTACAGAAAGGGCAAGGCCCTCAAGACAGACAGTATCTCTGCTTCTTCTTGC	839
OY	890	CTGCTGCTGCTCATATTTATGTGGGGATCAGCATGACTCTTTCATCTCTTTGGGAGTCAT	949
Db	840	CTGTGGGTGCTTACTATACATTTGGGATCAGATGACTCTTTCATCTCTTGGAAATCAT	899
OY	950	CAAACAAAGATGTACTTTCAGAGCAATTTGTGCACAGTGCATCTCCATCACAGAGCCCT	1009
Db	900	CAAACAAAGGCTGTAGTTTGAAGCACTGTGCACAGTGTGATTTCCATACACCGAGCCCT	959
OY	1010	CGCCTTCTTCACGTGTGCGGAAGCCCATCTCTATGCGTCTCTCGGGGGCAGTGTCAA	1069
Db	960	AGCTTTCTTCACGTGTGTGAAGCCCATCTCTTATGTCTTCTTGGAGCCAAATTTAA	1019
OY	1070	AAGCTCTGCCAGATGCACCTCAACTCCATGAGCAGAGGCTCAGACCTCAAGATCTCTTC	1129
Db	1020	AACCTCTGCCAGCAGCAGCACTCACTCTGTGAGCAGAGGCTCAGACCTCAAGATCTCTTC	1079
OY	1130	CAAGGAAAGGGGGTGACACTCTCCGTCGCCAGGAGTCAGAAATCTCCAGTTTCA	1189
Db	1080	CAAGGAAAGGGGGTGACACTCTCTGTTCCACTGAGCTGAGTCTTCAAGTTTCA	1139
OY	1190	CTCAGCAACCCCTTATGCCAAGACTTATATATATATATATATATATGATTAAGAACTT	1249
Db	1140	CTCAGCACTA-----CACAGATGTAAAGACTTTTATATATATATATATATATATAT	1191
OY	1250	TTTTTATGTACACATTTTCCAGATATAAGAGACTGACAGCTCTGACAGTTTATTTT	1309
Db	1192	TTTTTATGTACACATTTTTCAGATATATAAAGCACTGACCAATATTTGTAAGTTTATTC	1251
OY	1310	TTTTTATGTACTGTGGAGTTATATGTTCTCTAGTTTGTGAGGTTTACTTAATTT	1369
Db	1252	TTGTGTGATTTTGTGT-----CTGTGTCTTCTTATGTTTGTGAAGTTTATTTAGACTTA	1305
OY	1370	ATATATAATATGTTTTTTTGTGTTTCTATGTGATGAGCCGTCTGAGCAGACCTGTGGCC	1429
Db	1306	TTTTTATA-----TAAATTTTTTTTTTTTATATATATATGATGTGTCTGAGGCAAGCCGTGTGGCC	1361

1430 AAGTCTTAGTACGCTGTTATCTGTGTAGAGACTGTAGAGAGAACTGA 1489
1362 AAGTCTTAGTACGCTGTTATCTGTGTAGAGAGAACTGA 1413
1490 ACATCCAGATGCTGTGTAATGTAATAGTACGCTGTGTGTGCA 1549
1414 ACATCCAGATGCTGTGTAATGTAATAGTACGCTGTGTGTGCA 1473
1550 TAATCTCTCATTCGAGAGAGACCCACCCACCCACCCACCCATCTTAAT 1609
1474 TAGTAACTCTCA 1488
1610 TGTGTGTAGTACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1669
1489 TTTTCTGTAAAGTGCACCTTAACCAAGCTGTAATGTGTGTGTGTGTGT 1729
1526 TTTGCTGTAGAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1581
1730 TTTTGT 1789
1582 TTTTGT 1823
1790 GTACAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1849
1624 GTACAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1683
1850 AAAAAAAAAAAAAAAAAAAAAAAAAA 1877
1684 AAAAAAAAAAAAAAAAAAAAAAAAAA 1711

RESULT 8

US-08-801-228-3

Sequence 3, Application US/08801228

Patent No. 5922541

GENERAL INFORMATION:

APPLICANT: Lee, James

TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Winpalm (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/801,228

FILING DATE: 19-Feb-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/284586

FILING DATE: 10-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/076093

FILING DATE: 11-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/810782

FILING DATE: 19-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P0706P2P1D3

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-801-228-3

Query Match 51.9%; Score 974.4; DB 2; Length 1737;
Best Local Similarity 76.1%; Pred. No. 2.1e-187;
Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

50 GCAGGTAGCAGTACCTCTGAGGCGTTGCTGCGGTACACACCGGCTGTAGAG 109
20 GCGCGGCGCAAGTGTAGAGCGCGAGGCGCTGAGTGTCTCAGTAGCCACCGCATCTGGAGAG 79
110 GAGTGTGCTGAGTACCGTACGCTGAGTGTATATACATCTGTATACATCTGCAAGA 169
80 CAGCGGTACCATGGA-----GGGATCAGTATATATACATCTGTACAGTACACCGAGGA 134
170 AGTGGGCTGTGAGACTATGATCTCAACAAGAACCTGCTCCGGAGTGAAGAGTCCA 229
135 AATGGGCTCAGGGAGACTATGATCTCAACAAGAACCTGCTCCGGAGTGAAGAGTCCA 194
230 TTTCAATAGAGATCTTCTGCGCCACATCTATCATCTCTTCTGAGTGTGCTGCTGCTG 289
195 TTTCAATAGAGATCTTCTGCGCCACATCTATCATCTCTTCTGAGTGTGCTGCTGCTG 254
290 CAATGATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 349
255 CAATGATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 314
350 GTACAGGCTGACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 409
315 GTACAGGCTGACCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 374
410 AGTGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 469
375 AGTGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 434
470 CTACAGTGTACCTGTACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 529
435 CTACAGTGTACCTGTACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 494
530 CTTGCGCATTTGTCACGCCACCAACAGTCAAGGCCAAGAACCTGCTGCTGCTGCTGCTG 589
495 CTTGCGCATTTGTCACGCCACCAACAGTCAAGGCCAAGAACCTGCTGCTGCTGCTGCTG 554
590 AGTGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
555 AGTGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 614
650 CGAGCTGAGCAGGAGGAGATCAGTACAGGAGGAGTACAGTACATCTGAGCGCTTTGA 709
615 CAGG-----TCAGTGTAGGAGATGAGATATATCTGTGAGCGCTTTGA 659
710 CCGCATAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 769
660 CCGCATAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 719
770 GCGCGGATGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 829
720 GCGCGGATGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779
830 GCGCGGATGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 889
780 GCGCGGATGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839
890 CTG 949

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      840 CTGTGGCTGCGCTTACTACATGGGATCGACATCGACTCTTCATCTCTCGTAATCAT 899
      950 CAAGCAAGATGAGTGTGAGTGTGAGATGTGAGATGTGAGATGTGAGATGTGAGATGT 1009
      900 CAAAGCAAGGCTGTGAGTGTGAGATGTGAGATGTGAGATGTGAGATGTGAGATGT 959
      1010 CGGCTTCTTCACACTGTGCTGAGCAACCCCACTCTGATGCTTCTGCGGGCCAAAGTTCA 1069
      960 AGCTTCTTCACACTGTGCTGAGCAACCCCACTCTGATGCTTCTGAGCCAAATTTAA 1019
      1070 AAGCTTCTTCACACTGTGAGCAACCCCACTCTGATGCTTCTGAGCCAAATTTAA 1129
      1020 AAGCTTCTTCACACTGTGAGCAACCCCACTCTGATGCTTCTGAGCCAAATTTAA 1079
      1130 CAAAGCAAGGCTGTGAGTGTGAGATGTGAGATGTGAGATGTGAGATGTGAGATGT 1189
      1080 CAAAGCAAGGCTGTGAGTGTGAGATGTGAGATGTGAGATGTGAGATGTGAGATGT 1139
      1190 CTCACACTAACCTTATGCAAGACTTATATATATATATATATATATATATATATATAT 1249
      1140 CTCACACTAACCTTATGCAAGACTTATATATATATATATATATATATATATATATAT 1191
      1250 TTTTATGTTACACATTTTCCAGATATATAGAGACTGACAGCTGTGTACAGTTTTTTT 1309
      1192 TTTTATGTTACACATTTTCCAGATATATAGAGACTGACAGCTGTGTACAGTTTTTT 1251
      1310 TTTTATGTTACACATTTTCCAGATATATAGAGACTGACAGCTGTGTACAGTTTTTT 1369
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      1370 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1429
      1306 TTTTATGTTACACATTTTCCAGATATATAGAGACTGACAGCTGTGTACAGTTTTTT 1361
      1430 AAGTCTTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1489
      1362 AAGTCTTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1413
      1490 AATTCACAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1549
      1414 AATTCACAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1473
      1550 TATCTCTTCATTCAGAGAGACACCCACCACCCACCACCCACCACCATTTCTAAAT 1609
      1474 TAGATATCTCTCCA----- 1488
      1610 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1669
      1489 -----TTCGCGTGGAAAGCTTTTCTGCTGTCTTAAGACGTGAT 1525
      1670 TTTTCTGTAAGATGACACTTAAACCAAGGCTTAATGGGTGTGAGAAATCTGTGGGT 1729
      1526 TTTTCTGTAAGATGACACTTAAACCAAGGCTTAATGGGTGTGAGAAATCTGTGGGT 1581
      1730 TTTTCTGTAAGATGACACTTAAACCAAGGCTTAATGGGTGTGAGAAATCTGTGGGT 1789
      1582 -----TTTTCAGTTTCAGAGAGAGGCTGTGATTTTCAGACACCTTAC-AGT 1623
      1790 GTACACTCTGTGTATATATATATATATATATATATATATATATATATATATATATAT 1849
      1624 GTACACTCTGTGTATATATATATATATATATATATATATATATATATATATATATAT 1683
      1850 AAAAAAAAAAAAAAAAAAAAAAAAAA 1877
      1684 AAAAAAAAAAAAAAAAAAAAAAAAAA 1711

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RESULT 9
 US-09-104-296-3
 ; Sequence 3, Application US/09104296
 ; Patent No. 6087475
 ; GENERAL INFORMATION:

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      ? APPLICANT: Lee, James
      ? APPLICANT: Wood, William I.
      ? TITLE OF INVENTION: PF4A Receptors
      ? NUMBER OF SEQUENCES: 6
      ? CORRESPONDENCE ADDRESS:
      ? ADDRESSEE: Genentech, Inc.
      ? STREET: 1 DNA Way
      ? CITY: South San Francisco
      ? STATE: California
      ? COUNTRY: USA
      ? ZIP: 94080
      ? COMPUTER READABLE FORM:
      ? MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
      ? COMPUTER: IBM PC compatible
      ? OPERATING SYSTEM: PC-DOS/MS-DOS
      ? SOFTWARE: Winpatin (Genentech)
      ? CURRENT APPLICATION DATA:
      ? APPLICATION NUMBER: US/09/104,296
      ? FILING DATE: 24-June-1998
      ? CLASSIFICATION:
      ? PRIOR APPLICATION DATA:
      ? APPLICATION NUMBER: 08/701265
      ? FILING DATE: 22-AUG-1996
      ? PRIOR APPLICATION DATA:
      ? APPLICATION NUMBER: 08/664228
      ? FILING DATE: 06-JUN-1996
      ? PRIOR APPLICATION DATA:
      ? APPLICATION NUMBER: 08/076093
      ? FILING DATE: 11-JUN-1993
      ? PRIOR APPLICATION DATA:
      ? APPLICATION NUMBER: 07/810782
      ? FILING DATE: 19-DEC-1991
      ? ATTORNEY/AGENT INFORMATION:
      ? NAME: Love, Richard B.
      ? REGISTRATION NUMBER: 34,659
      ? REFERENCE/DOCKET NUMBER: P07062C2
      ? TELECOMMUNICATION INFORMATION:
      ? TELEPHONE: 415/225-5530
      ? TELEFAX: 415/952-9881
      ? TELEX: 910/371-7168
      ? INFORMATION FOR SEQ ID NO: 3:
      ? SEQUENCE CHARACTERISTICS:
      ? LENGTH: 1737 base pairs
      ? TYPE: Nucleic Acid
      ? STRANDEDNESS: Single
      ? TOPOLOGY: Linear
      ? US-09-104-296-3
      ?
      ? Query Match 51.9%; Score 974.4; DB 3; Length 1737;
      ? Best Local Similarity 76.1%; Pred. No. 2.1e-187;
      ? Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;
      ?
      ? 50 GCAGGTGAGTGAACCTCTGAGGCTTGTGCTCCGTTAAACACACGAGGTGTAGAC 109
      ? 20 GCGCGCGCAAGTGTGAGGCGGAGGCGCTGAGTGTCCAGTAGGACACCGATGTGGAGAC 79
      ? 110 GAGTGTGCGCATGGAACCATCATGAGTGTATATACCTTCTGATTAATCTGTGAAGA 169
      ? 80 CAGCGGTACCATGGA-----GGGATCAGTATATACCTTTCAGATTAATACCGAGGA 134
      ? 170 AGTGGGCTGTGAGATGTATGACTCCAAACAAGAACCTCTTCGCGGATGGAAGACGTCA 229
      ? 135 AATGGGCTCAGGGGACTATGACTCCATGAAGAACCTCTTTCGCGGATGGAAGACGTCA 194
      ? 230 TTTCAATTAATCTTCTGCGCACCATCTATCTCATCTTCTTAAGTGTGAGTGTGG 254
      ? 290 CAATGATGTGTGATCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 289
      ? 255 CATGTGATGTGTGATCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 314
      ? 350 GTACCGGCTGACACTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 409

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Db 315 GTACAGGCTGCACCTGTCACGTGGCCGACCTCTTGTGTCATCAGCCTTCCTTGCGGC 374
QY 410 AGTGTATGCCATGGCTGACGTGTACTTTGGGAAATTTTGTGAAGCTCTCCATATCAT 469
Db 375 AGTTGATGCCGTGCAAACTGTGTACTTTGGAACTTCTTAATGGAAGCACTCATGTGCAT 434
QY 470 CTACACTGTCTAACCTCTACAGCAGCTTCATCTGCGCTTCATCAGCTCGAGCGGTA 529
Db 435 CTACAGAGTCAACCTCTACAGCAGTGTCTCATCTGCGCTTCATCAGTGTGAGCCGCTA 494
QY 530 CTTGCCATTTGTCCAGGCCACCAACAGTCAAGGCCAAGAACTGCTGCTGAAAAGC 569
Db 495 CCGGCGATCTGTCACAGCCACCAACAGTCAAGGCCAAGAACTGCTGCTGAAAAGT 554
QY 590 AGTCTATGTGGGGTGTGATGCCAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
Db 555 GGTCTATGTGGGGTGTGATGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 614
QY 650 CGACGTACAGCCAGGGGACATCAGTACAGGGGATGACAGTACATCTGTGACCCGCTTGA 709
Db 615 CAACG-----TCACTGAGGAGATGACAGTATATCTGTGACCGCTTCTA 659
QY 710 CCCCAGATAGCTGTGATGTGTGCTTCAATTCAGACATATAATGTGGTCTGATCT 769
Db 660 CCCCAGATAGCTGTGATGTGTGCTTCAATTCAGACATATAATGTGGTCTGATCT 719
QY 770 GCGCGGATGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 829
Db 720 GCTGTGATGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 779
QY 830 GGGCCACAGAACGCGAAGGCCCTCAAGAGACAGTATCTGATCTGCTGCTGCTGCTG 889
Db 780 GGGCCACAGAACGCGAAGGCCCTCAAGAGACAGTATCTGATCTGCTGCTGCTGCTG 839
QY 890 CTGCTGGCTGCCATTAATGTGGGATCAGCATCAGTCTCTTATCTTTGGAGTCA 949
Db 840 CTGTTGGCTGCCATTAATGTGGGATCAGCATCAGTCTCTTATCTTTGGAGTCA 899
QY 950 CAAGCAAGATGTGACTGTGAGCATTTGTCAGCAAGTGTGATCTGATCTGATCTGATCT 1009
Db 900 CAAGCAAGATGTGACTGTGAGCATTTGTCAGCAAGTGTGATCTGATCTGATCTGATCT 959
QY 1010 CGCTTCTTTCAGTGTGTGCTGAACCCATCTCTATGCTTCTGCGGCGCAAGTTC 1069
Db 960 AGCTTCTTTCAGTGTGTGCTGAACCCATCTCTATGCTTCTGAGCCAAATTTA 1019
QY 1070 AAGCTCTGCCAGCATGCACTCACTCATGACAGAGCTCCAGCTCAAGTCTTTC 1129
Db 1020 AAGCTCTGCCAGCATGCACTCACTCATGACAGAGCTCCAGCTCAAGTCTTTC 1079
QY 1130 CAAGGAAAGCGGGGAGACACTCTTCCGTCACGAGAGTGAATCCCTGAGTTTCA 1189
Db 1080 CAAGGAAAGCGGGGAGACACTCTTCCGTCACGAGAGTGAATCCCTGAGTTTCA 1139
QY 1190 CTCCAGCTAACCTTATGCAAGACTTAATAATATATATATATATATATATATATAT 1249
Db 1140 CTCCAGCTAACCTTATGCAAGACTTAATAATATATATATATATATATATATATAT 1191
QY 1250 TTTTATGTATACATTTTCCAGATATAAGAGACTGACCACTTTGTACAGTTT 1309
Db 1192 TTTTATGTATACATTTTCCAGATATAAAGAGACTGACCAATTTGTACAGTTT 1251
QY 1310 TTTTATGTATACATTTTCCAGATATAAGAGACTGACCACTTTGTACAGTTT 1369
Db 1252 TTTTATGTATACATTTTCCAGATATAAAGAGACTGACCAATTTGTACAGTTT 1305
QY 1370 ATATAAATATATTTTGTGTTTGTATGATGATGATGATGATGATGATGATGATGATG 1429
Db 1306 TTTTATATATATTTTGTGTTTGTATGATGATGATGATGATGATGATGATGATGATG 1361
QY 1430 AAGTTCTAGTACGTTTATCTGCTGATGAGACTGATGAGAGAGAACTGA 1489
Db 1430 AAGTTCTAGTACGTTTATCTGCTGATGAGACTGATGAGAGAGAACTGA 1489

Db 1362 AAGTTCTAGTACGTTTATCTGCTGATGAGACTGATGAGAA-----AAGGAACTGA 1413
QY 1490 ACATTCAGAGATGTGTGTAATAATGAATGAAGCTAGCCGATCCTGATGCTGTGCA 1549
Db 1414 ACATTCAGAGATGTGTGTAATAATGAATGAAGCTAGCCGATGATGCTGTGCA 1473
QY 1550 TAATCTCTTATCTCCAGAGGACACCCACCACCCACCCACCCACCCACCCATTTTAAAT 1609
Db 1474 TAGATATCTCTCA----- 1488
QY 1610 TGTGTGTATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1669
Db 1489 -----TTCGCGGAGACCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1525
QY 1670 TTTTCTGTAAGAATGACCTTAAACCAAGCTGAATGATGATGATGATGATGATGATG 1729
Db 1526 TTTGCTGTAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1581
QY 1730 TTTTGT 1789
Db 1582 -----TTTTCAGTTTCAGAGAGTGGGTGATTTTCAGACACCTTAC-AGT 1623
QY 1790 GTACAGTCTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1849
Db 1624 GTACAGTCTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1683
QY 1850 AAAAAAAAAAAAAAAAAAAAAAAAAA 1877
Db 1684 AAAAAAAAAAAAAAAAAAAAAAAAAA 1711

RESULT 10
PCT-US94-06380-2
; Sequence 2, Application PC/TUS9406380
; GENERAL INFORMATION:
; APPLICANT: Chundharpai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: K. Jin Kim
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY DISORDERS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706F2P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 bases
; TYPE: nucleic acid

CURRENT FILING DATE: 2000-03-02
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 14
 LENGTH: 1679
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-517-605-14

Query Match 50.8%; Score 952.8; DB 4; Length 1679;
 Best Local Similarity 80.2%; Pred. No. 4,6e-183;
 Matches 120; Conservative 0; Mismatches 252; Indels 46; Gaps 6;

44 GGAGGTGACAGTACAGTACCTCTGAGACCTTTGGCTCTCGGTACACACCGGCTG 103
 12 GGGGACGACAGTACAGTACGAGGAGGCTGAGTCTCCAGTACGACCGGCTG 71
 104 TAGAGGAGTGTGGCCATGGAACCGATCAGTGTATATACATCTTGTATATCTC 163
 72 GAGAACACGCGTTACATGGA-----GGGATCAGATATATACATCTTGTATATCTC 126
 164 TGAGAGTGGGGTGGAGTACATGATCCAAACAGGAAACCTGCTTCCGGATGAAA 223
 127 CGAGGAAATGGGCTGAGGAGTATGATCCATGAGGAAACCTGTTCCGTAAGAAA 186
 224 CGTCAATTCATAGGATCTTCTGCGCCACATCTACTTATCATCTTCTGACTGGCAT 283
 187 TGTATATTCATATAATATCTCTCTGCGCCACATCTACTTATCATCTTCTGACTGGCAT 246
 284 AGTGGCAATGATGTTGGTGTCTGATGATGATGATGATGATGATGATGATGATGAT 343
 247 TGTGGGCAATGATGTTGGTGTCTGATGATGATGATGATGATGATGATGATGATGAT 306
 344 GGACAGTACCGGCTGACCTGATGATGATGATGATGATGATGATGATGATGATGAT 403
 307 GGCAGATGACAGGCTGACCTGATGATGATGATGATGATGATGATGATGATGATGAT 366
 404 CTGGGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 463
 367 CTGGGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426
 464 TATCATCTACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 523
 427 TGTCACTCTACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 486
 524 CCGGATCTGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 583
 487 CCGGATCTGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 546
 584 AAAGGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 643
 547 AAAGGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 606
 644 CTTTGGCAGCTACAGCAGGAGGAGATGATGATGATGATGATGATGATGATGATGATGAT 703
 607 CTTTGGCAGC-----TCAGTGGGAGATGATGATGATGATGATGATGATGATGATGATGAT 651
 704 CTTTACCCGATAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 763
 652 CTTTACCCGATAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 711
 764 CATCTGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 823
 712 TATCTGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771
 824 CTCGAAGGCGCACAGAGCGGCTCAAGACGATGATGATGATGATGATGATGATGATGATGAT 883
 772 CTCGAAGGCGCACAGAGCGGCTCAAGACGATGATGATGATGATGATGATGATGATGATGAT 831
 884 CTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943
 832 CTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 891

944 AGTCAACAGCAGAGTGTGACTGTGAGACATGTCAGAGTGTGATGATGATGATGATGATGAT 1003
 892 AATCATCAAGCAGAGGTTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 951
 1004 GGCCTGCGCTTCTTCCACTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1063
 952 GGCCTGAGCTTCTTCCACTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1011
 1064 GTTCAAAAGCTGCTGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1123
 1012 ATTTAAACCTTCTGCGCAGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1071
 1124 CTTTCCAAAGGAAAGCGGGGTGAGACATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1183
 1072 CCTTCGCAAGGAAAGCGGGGTGAGACATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1131
 1184 TTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1243
 1132 TTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1183
 1244 GAACTTTTATGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1303
 1184 ACTTTTATGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1243
 1304 TTTTATGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1363
 1244 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1297
 1364 TATTTATGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1423
 1298 GACTTATTTATA-----TAAATTTTGTGTTTCAATGATGATGATGATGATGATGATGATGAT 1353
 1424 GTGGCAAGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1483
 1354 GTGGCAAGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1405
 1484 AACTGAACATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543
 1406 AACTGAACATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1465
 1544 GCTGCATA 1551
 1466 TATGATA 1473

RESULT 12
 US-09-582-224A-5
 Sequence 5, Application US/0958222A
 Patent No. 6429308
 GENERAL INFORMATION:
 APPLICANT: IJIMA, Osamu
 APPLICANT: GOTO, Takeshi
 APPLICANT: SHIMADA, Takashi
 TITLE OF INVENTION: HIV Infection Inhibitors
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/09/582,224A
 CURRENT FILING DATE: 2000-07-21
 PRIOR APPLICATION NUMBER: PCT/JP99/06534
 PRIOR FILING DATE: 1999/11/24
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: Microsoft Word
 SEQ ID NO 5
 LENGTH: 1664
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: cDNA of CXCR4
 US-09-582-224A-5

Query Match 50.7%; Score 951.8; DB 4; Length 1664;
 Best Local Similarity 80.2%; Pred. No. 7,3e-183;
 Matches 120; Conservative 0; Mismatches 252; Indels 46; Gaps 6;

QY 45 CAGTCAGGTAGCAGTGCCTCTGAGGGCTTGTGCTCCGGTAACCAACGCGCTG 104
1 CGGAGCAGAGGTAAGTGCAGCGGCGTGTGCTCCAGTACCGCATCTGG 60
QY 105 AGAGCGAGTGTGCGATGGAACCGATGATGTGATATATACCTTTGATTA 164
61 AGAACCGCGGTATCCATGGA-----GGGATCAGTATATACCTTCAGTAACTACACC 115
QY 165 GAAGAACTGGGGTGTGAGACTATGACTTCCAGCAAGACCCCTGTCGGGATGAAC 224
116 GAGAAATGGGCTTCAGGAGCTATGACTCCATGAGAAACCCCTTTCCGGAAGAAAT 175
QY 225 GTCCATTTCAATAGATCTTCCTGCCCCACCATCTACTTCACTCTTCTGACTGCATA 284
176 GCTAATTTCAATAAATCTTCCTCCACCATCTACTTCACTCTTCACTTAACTGCAAT 235
QY 285 GTGGCAATGATGTGGATCTGCTGCTGATGGGTTACCAAGAAAGCTAAGAGATACG 344
236 GTGGCAATGATGTGGATCTGCTGCTGATGGGTTACCAAGAAAGCTAAGAGATACG 295
QY 345 GACAACTACCGGCTGCACCTGTGAGTGGCTGACCTCTTGTGATCACACTCCCTTC 404
296 GACAACTACCGGCTGCACCTGTGAGTGGCTGACCTCTTGTGATCACACTCCCTTC 355
QY 405 TGGCAGTGTATGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
356 TGGCAGTGTATGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 415
QY 465 ATCATCTACACTGTCAACCTCTACAGAGGCTTCTCATCTGCGCTTCAAGCTGAC 524
416 GTCATCTACACTGTCAACCTCTACAGAGGCTTCTCATCTGCGCTTCAAGCTGAC 475
QY 525 CGATACCTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584
476 CGATACCTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 535
QY 585 AAGCAGCTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 644
536 AAGCAGCTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 595
QY 645 TTTGCCAGCTGACAGCGAGGAGATAGTACAGGAGATGACAGTACATCTGACCGC 704
596 TTTGCCAGCTGACAGCGAGGAGATAGTACAGGAGATGACAGTACATCTGACCGC 640
QY 705 CTTTACCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 764
641 TTTTACCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 700
QY 765 ATCTGCGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
701 ATCTGCGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 760
QY 825 TCCAAAGGCGCAGCAAGGCGGCTCAAGAGCAGAGTACATCTGACCTTTC 884
761 TCCAAAGGCGCAGCAAGGCGGCTCAAGAGCAGAGTACATCTGACCTTTC 820
QY 885 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 944
821 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880
QY 945 GTCATCAAGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1004
881 ATCATCAAGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 940
QY 1005 GCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1064
941 GCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1000
QY 1065 TTTCAAAAGCTTGGCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1124
1001 TTTTAAAGCTTGGCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1060
QY 1125 CTTTCAAAAGGAAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1184

Db 1061 CTTTCAAAAGGAAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1120
QY 1185 TTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1244
Db 1121 TTTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1172
QY 1245 AACTTTTATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1304
1173 CTTTTTTATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1232
QY 1305 TTTTTTTATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1364
1233 ATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1286
QY 1365 AATTATATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1424
Db 1287 ACTTATATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1342
QY 1425 TGGCAGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1484
Db 1343 TGGCAGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1394
QY 1485 ACTGACATTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1544
Db 1395 ACTGACATTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1454
QY 1545 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1551
Db 1455 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1461

RESULT 13

US-08-153-848-45

Sequence 45, Application US/0813848

Patent No. 5759804

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald

APPLICANT: Gray, Patrick W.

APPLICANT: Schweikart, Vicki L.

TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/153,848

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 5759804and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 1317 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 201..1211
US-08-153-848-45

Query Match 44.5%; Score 834.6; DB: 1; Length 1317;
Best Local Similarity 83.9%; Pred. No. 2,66-159;
Matches 977; Conservative 0; Mismatches 164; Indels 24; Gaps 2;

QY 134 TGTGAGTATATACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 193
DB 164 TTTGAGATATACACTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 223
QY 194 CAACAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 253
DB 224 CATGAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 283
QY 254 CATCTACTTCTGATTAATCTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 313
DB 284 CATCTACTTCTGATTAATCTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 343
QY 314 GGGTTACAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 373
DB 344 GGGTTACAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 403
QY 374 TGACCTCTCTTGTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 433
DB 404 CGACCTCTCTTGTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 463
QY 434 CTGTTGGAAATTTTGTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 493
DB 464 CTGTTGGAAATTTTGTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 523
QY 494 CGTTCTGATTAATCTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 553
DB 524 TGTCTCTGATTAATCTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 583
QY 554 CAGTCAAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 613
DB 584 CAGTCAAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 643
QY 614 AGCCCTCTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 673
DB 644 TGCCCTCTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 688
QY 674 TCAGGGGAGATGACAGTATCTGAGAAAGTGGCTGTGAGACTATGACTC 733
DB 689 TGAGGAGATGACAGTATCTGAGAAAGTGGCTGTGAGACTATGACTC 748
QY 734 GTTTCATTTGACAGTATCTGAGAAAGTGGCTGTGAGACTATGACTC 793
DB 749 GTTTCATTTGACAGTATCTGAGAAAGTGGCTGTGAGACTATGACTC 808
QY 794 TTACTGATCATCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 853
DB 809 CTATTGATCATCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 868
QY 854 CAAGAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 913
DB 869 CAAGAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 928
QY 914 GATGAGATGACAGTATCTGAGAAAGTGGCTGTGAGACTATGACTC 973
DB 929 GATGAGATGACAGTATCTGAGAAAGTGGCTGTGAGACTATGACTC 988
QY 974 CATGTCAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 1033
DB 989 CATGTCAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 1048

QY 1034 CCCATCCTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 1093
DB 1049 CCCATCCTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 1108
QY 1094 CTGTCAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTC 1153
DB 1109 CTGTCAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTC 1168
QY 1154 TTGCGTCTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTATGACTC 1213
DB 1169 ATCTGTCAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTC 1226
QY 1214 CTGTCAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTC 1273
DB 1227 AGACTTTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTC 1279
QY 1274 ATGAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTC 1298
DB 1280 ATGAGAGAACCTTCTGATTAATCTCTGAGAAAGTGGCTGTGAGACTC 1304

RESULT 14

US-09-299-843A-45
Sequence 45, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: JILL E. UHL
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 201..1211
US-09-299-843A-45

Query Match 44.5%; Score 834.6; DB 3; Length 1317;
Best Local Similarity 83.9%; Pred. No. 2.6e-159;
Matches 977; Conservative 0; Mismatches 164; Indels 24; Gaps 2;

134 TGTGATATATACACTTCTGATACACTCTCTGAGAGAGTGGGGTGGAGACTATGACTC 193
164 TTTCGAGATATATACACTTCTGATACACTCTCTGAGAGAGTGGGGTGGAGACTATGACTC 223
194 CAAGAAGAACTCTGCTTCCGAGTAAAGAGTCCATTTTCATATAGATCTCTCTGAGAG 253
224 CATGAGAAAGCTCTGCTTCCGAGTAAAGAGTCCATTTTCATATATATATCTCTGAGAG 283
254 CATCTACTCTATATCTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 313
284 CATCTACTCTATATCTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 343
314 GGGTTACAGAGAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 373
344 GGGTTACAGAGAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 403
374 TGACCTCTCTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 433
404 CGACCTCTCTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 463
434 CTCTTGGAAATTTTGTGATAGCTCTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAG 493
464 CTCTTGGAAATTTTGTGATAGCTCTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAG 523
494 CGTTCTACCTCTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 553
524 TGCTCTACCTCTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 583
554 CAGTCAAGAGAGAGAGTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 613
584 CAGTCAAGAGAGAGAGTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 643
614 AGGCTCTCTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 673
644 TGCTCTACCTCTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 693
674 TCAGGGAGAGAGAGTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 723
689 TGAGGAGAGAGAGAGTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 748
734 GTTTCATTTCCAGATATATATGAGTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTG 793
749 GTTTCATTTCCAGATATATATGAGTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTG 808
794 TTACTGATATATATCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 833
809 CTATTCATTTATATCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 868
854 CAAGAGAGAGAGAGTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 913
869 CAAGAGAGAGAGAGTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 928
914 GATCAGAGAGAGAGTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 973
929 GATCAGAGAGAGAGTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 988
974 CATTTGAGAGAGAGTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 1033
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1214 CTAT 1273
1227 -----AGACTTTTAT 1279
1274 ATAGAGAGTCTGAGTCTGATACACTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 1298
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RESULT 15
US-09-088-337B-45
Sequence 45, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-Nov-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-Nov-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 201..1211
SEQUENCE DESCRIPTION: SEQ ID NO: 45;
US-09-088-337B-45
Query Match 44.5%; Score 834.6; DB 4; Length 1317;
Best Local Similarity 83.9%; Pred. No. 2.6e-159;
Matches 977; Conservative 0; Mismatches 164; Indels 24; Gaps 2;

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Qy	1274		ATAAGAGACTGACCAGTCTGTACA	1298
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Search completed: July 12, 2003, 16:00:12
Job time : 90 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 16:00:18 ; Search time 2185 seconds

(without alignments)
4781.651 Million cell updates/sec

Title: US-09-367-052-2

Perfect score: 1867
Sequence: 1 MEPIVSIVSYSDNYSEEVGS.....KRGHSSVSSESSSFHSS 359

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model DEV=xlh
-O=/cgn2_1/USPTO.spool/US09367052/runat_10072003-100044-10351/app-query.fasta-1.519
-DB=GenDbml -OFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS-human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09367052 -CGN_1_1-1687 -ernat_10072003-100044-10351 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEOBFRY -NES.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOGS
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database :

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14: gb_vi:*
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16: em_fun:*
17: em_hum:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1867	100.0	1223	10	MMU59760
2	1867	100.0	1817	10	BC031665
3	1867	100.0	1877	10	D87747
4	1866	99.9	1575	10	MMLESTRPT
5	1866	99.9	1809	10	AB000803
6	1848	99.0	1180	10	MMLCR12
7	1836	98.3	1422	10	MMLCR13
8	1836	98.3	3366	10	MMU65580
9	1835	98.3	3770	10	MMLESTRGN
10	1758.5	94.2	1050	10	AF452185
11	1744.5	93.4	1050	10	RNU90610
12	1686.5	90.3	1059	9	AF031089
13	1683.5	90.2	1087	9	AF001928
14	1679.5	90.0	1068	9	AB015943
15	1679.5	90.0	1078	9	D86579
16	1678.5	89.9	1044	9	AF172234
17	1678.5	89.9	1059	6	AX256185
18	1678.5	89.9	1059	6	AX482330
19	1678.5	89.9	1059	9	AF025375
20	1678.5	89.9	1087	9	PTU89798
21	1678.5	89.9	1225	9	HUMNYRECA
22	1678.5	89.9	1637	9	HUMNSTR
23	1678.5	89.9	1645	9	HSNPTFLA
24	1678.5	89.9	1664	6	E37853
25	1678.5	89.9	1664	9	HUMHMB9
26	1678.5	89.9	1664	11	G28514
27	1678.5	89.9	1670	6	AX409496
28	1678.5	89.9	1670	9	HUMGPCR
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32	1678.5	89.9	1737	6	AR060748
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44	1676.5	89.8	1044	9	AF172218
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RESULT 1

ALIGNMENTS

MMU59760 1223 bp mRNA linear ROD 09-SEP-1996
LOCUS MMU59760
DEFINITION Mus musculus fusin homolog mRNA, complete cds.
ACCESSION U59760
VERSION U59760.1 GI:1527134
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1223)
Heesen, M., Berman, M.A., Gerard, C. and Dorf, M.E.
Cloning of the mouse homologue of the human HIV co-factor gene,
fusin
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1223)
AUTHORS Heesen, M., Berman, M.A., Gerard, C. and Dorf, M.E.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1996) Pathology, Harvard Medical School, 200
Longwood Avenue, Boston, MA 02115, USA
LOCATION/Qualifiers
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/db_xref="taxon:10090"
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BASE COUNT 285 a 342 c 268 g 328 t
ORIGIN
Alignment Scores:
Pred. No.: 2.73e-178 Length: 1223
Score: 1867.00 Matches: 359
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Gaps: 0
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QY 81 HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTTPAlaValAspAla 100
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QY 101 MetaIaasPTryrrPheGlyLysPheLeuGlyLysAlaValHisIleIleTyrrThVal 120

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QY 121 AsnLeuTyrrSerSerValIleLeuAlaPheIleSerLeuAspArgTyrrLeuAlaIle 140
DB 390 AACCTCTACAGCAGCGTTCATCTCTGCTGCTTCATCAGCCCTGGACCGGTACTTCGCATT 449
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DB 450 GTCCAGCCGACACATCATCAAGGCCAAGAACTGCTGGCTGAAAGGAGTATATCTG 509
QY 161 GlyValTyrrIleProAlaLeuLeuThrIleProAspPheIlePheAlaAspValSer 180
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QY 181 GlnGlyAspIleSerGlnGlyAspAspArgTyrrIleCysAspArgLeuTyrrProAspSer 200
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DB 630 CTGTGATGTGTGTGTTTCAATTCACCATATATGATGGGTCTCATCTCCCGGATC 689
QY 221 ValIleLeuSerCysTyrrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGln 240
DB 690 GTCATCTCTCTCTGTACTGATCATCATCTCCAAAGCTGTACACTCAAGGGCCACACAG 749
QY 241 LysArgLysAlaLeuLysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrrLeu 260
DB 750 AAGCGCAAGGCCCTCAAGACAGACAGTATCTCTATCTCTTCTTGTGCTGTGGCTG 809
QY 261 ProTyrrTyrrValGlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGly 280
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QY 281 CysAspPheGluSerIleValHisLysTyrrIleSerIleThrgluAlaLeuAlaPhe 300
DB 870 TGTACTCTCGAGACATCTGACACAAAGTGTATCTCATCTCAGAGGCCCTCGCTCTTC 929
QY 301 HisCysCysLeuAsnProIleLeuTyrrAlaPheLeuGlyAlaLysPheLysSerSerAla 320
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QY 321 GlnHisAlaLeuAsnSerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLys 340
DB 990 CAGCATGACATCACTCATGASAGACAGGCTCCAGCTCAAGATCTTCCAAAGAAAG 1049
QY 341 ArgGlyGlyHisSerSerValSerThrgluSerGluSerSerSerPheHisSerSer 359
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RESULT 2
BC031665 1817 bp mRNA linear ROD 07-AUG-2002
LOCUS BC031665
DEFINITION Mus musculus, chemokine (C-X-C) receptor 4, clone MGC:36266
IMAGE:3592479, mRNA, complete cds.
ACCESSION BC031665
VERSION BC031665.1 GI:21618781
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1817)
Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amgdbcm.tmc.edu
 Guarante: P.H., Garcia, A.M., Lu, X., Huylk, S.W., Hale, S.M.,
 Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LIML at: <http://image.liml.gov>
 Series: IRAX Plate: 61 Row: d Column: 24
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Similarity but not
 identity to protein.

FEATURES

Location/Qualifiers
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 model. 10 month old virgin mouse. Taken by biopsy."
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 78..1157
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 GVMIPALLITPDIFFADVSOGDISGDDRYICDRLYPSDLMVAVFOFOHIMVGLIP
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CDS

BASE COUNT 443 a 435 c 396 g 543 t
 ORIGIN

Alignment Scores:

Pred. No.: 4.23e-178 Length: 1817
 Ent: 1867.00 Matches: 359
 Local Similarity: 100.00% Conservative: 0
 Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DE: 10 Gaps: 0

US-09-367-052-2 (1-359) x BC031665 (1-1817)

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 Oy 21 GlysApTYrAspSerAsnLysGluProCysPheArgAspGluAsnValHisPheAsnArg 40
 Db 138 GGAGACTATGACTCAACAGAAACCCGCTTCGGGATGAAGAAAGCTCATTTCAATGAG 197
 Oy 41 IlePheLeuProThrIleTyRPhelIleIlePheLeuThrGlyIleValAlGlyAsnGlyLeu 60
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 Oy 81 HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAla 100

Db 318 CACCTGTCAGTGGCTGACCTCTCTTGTGATCAACACACTCCCTTCTGGGAGTTGATGCC 377
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 Oy 241 LysArgLysAlaLeuLysThrValIleLeuIleLeuAlaPheAlaCysTrpLeu 260
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 Db 918 TGTGATCTGAGAGCATTTGTGCACAAAGTATCTTCAACAGAGAGCCCTGCTTCTTC 977
 Oy 301 HisCysLysLeuAsnProIleLeuTyRAlaPheLeuGlyAlaLysPheLysSerSerAla 320
 Db 978 CACTGTTCCTGAGAACCCCATCTCTATGCTTCTTCTGCGGCGCAAGTCAAAAGCTCTGCC 1037
 Oy 321 GlnHisAlaLeuAsnSerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLys 340
 Db 1038 CAGCATGCACTCAACTCATGAGCAGAGGCTTCACAGCTTCAAGATCCCTTCCAAAGCAAG 1097
 Oy 341 ArgGlyGlyHisSerSerValSerThrLysSerGluSerSerSerPheHisSerSer 359
 Db 1098 CGGGGTGACACTCTTCTGCTCCAGGAGTCAAGATCTTCAAGTTCCTCACTCCAGC 1154

RESULT 3
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 LOCUS D87747
 DEFINITION Mus musculus mRNA for murine CXCR-4, complete cds.
 ACCESSION D87747
 VERSION D87747.1 GI:1772445
 KEYWORDS murine CXCR-4.
 SOURCE Mus musculus bone marrow pre-B cell cell_line:DW34 cDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (sites)
 Nagasawa, T., Nakajima, T., Tachibana, K., Itasaka, H., Bleul, C.C.,
 Yoshie, O., Matsushima, K., Yoshida, N., Springer, T.A. and
 Kishimoto, T.
 Molecular cloning and characterization of a murine pre-B-cell
 growth-stimulating factor/stromal cell-derived factor 1 receptor, a
 murine homolog of the human immunodeficiency virus 1 entry
 coreceptor fusin

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (25), 14726-14729 (1996)
 MEDLINE 97121456
 REFERENCE 2 (bases 1 to 1877)
 AUTHORS Nagasawa, T.
 TITLE Molecular cloning of murine PBSF/SDF-1 receptor
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1877)
 AUTHORS Nagasawa, T.
 TITLE Direct Submission
 JOURNAL Submitted (05-SEP-1996) Takashi Nagasawa, Research Institute, Osaka
 Medical Center, Department of Immunology, Murdoccho 840, Izumi,
 Osaka 590-02, Japan (E-mail: immunol@osk.riwwebnet.or.jp,
 Tel: 0725-56-1220, Fax: 0725-57-3021)
 Location/Qualifiers

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gene
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BASE COUNT 469 a 450 c 407 g 551 t
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Alignment Scores:

Pred. No.: 4.38e-178 Length: 1877
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 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

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 Oy 61 ValIleLeuValMetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeu 80
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 Db 360 CACGTCGATGGGCGATGACCTCTCTTCTCATACACATCCCTCTCGGAGATGATGCC 419
 Oy 101 MetAlaAspTyrPheGlyLysPheLeuGlyLysAlaValHisIleIleTyrThrVal 120
 Db 420 ATGGCTGACTGCTACTTGGGAAATTTTGTGTAAAGGCTGTCCATATCATCTACAGTGC 479

Oy 121 AsnLeuTyrSerSerValIleuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIle 140
 Db 480 AACCTCTACAGACACCGTCTTCATCTGCTTATACAGCTTGACCGGCTACCTCGCATTT 539
 Oy 141 ValHisAlaThrAsnSerGlnArgProArgLysLeuLeuAlaGlyLysAlaValTyrVal 160
 Db 540 GTCACCGCCACCAACACTCAAGGCCCAAGAAACTGCTGCTGCTGCTGCTGCTGCTGCTG 599
 Oy 161 GlyValThrIleProAlaLeuLeuThrIleProAspPheIlePheAlaAspValSer 180
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 Oy 181 GlnGlyAspIleSerGlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSer 200
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 Oy 201 LeuTrpMetValValPheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIle 220
 Db 720 CTGTGATGGTGGTGTTCATATCCACATATATATGATGGGTCTCATCTCCCGGCATC 779
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 Db 780 GTCATCT 839
 Oy 241 LysArgLysAlaLeuLysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrLeu 260
 Db 840 AAGGCGACAGCGCCCTCAAGACAGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 899
 Oy 261 ProTyrTyrValGlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGly 280
 Db 900 CCATATATATGGGGATCAGACATCGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 959
 Oy 281 CysAspPheGluSerIleValHisLysThrIleSerIleThrGlnAlaAlaPhePhe 300
 Db 960 TGTACTTCGAGACATGTGACAAATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1019
 Oy 301 HisCysCysLeuAsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAla 320
 Db 1020 CACTGTTCGTCGACCCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1079
 Oy 321 GlnHisAlaLeuAsnSerMetSerArgLysSerIleLeuSerLysGlyLys 340
 Db 1080 CAGCATCACCACTCATGATGAGCAGAGGCTCCAGCTTCCAAAGATCTTCCAAAGGAAG 1139
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 Db 1140 CGGGGTGACACT 1196

RESULT 4
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 LOCUS M.musculus mRNA for leukocyte-derived seven transmembrane domain
 DEFINITION receptor.
 ACCESSION X99582.1 GI:1666648
 VERSION X99582.1 GI:1666648
 KEYWORDS leu gene; leukocyte-derived seven transmembrane domain receptor.
 SOURCE Mus musculus.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1575)
 REFERENCE Moeppe, B., Frodl, R., Kessler, H. and Gierschik, P.
 cDNA cloning and genomic organization of a leukocyte-derived seven
 transmembrane domain receptor (LESTR) from mouse: a murine
 homologue of the human HIV-1 entry cofactor fusin
 Unpublished
 JOURNAL 2 (bases 1 to 1575)
 REFERENCE Moeppe, B.
 AUTHORS Moeppe, B.
 TITLE Direct Submission
 JOURNAL Submitted (19-JUL-1996) B. Moeppe, Universitaet Ulm,
 Pharmacology/Toxicology, Albert-Einstein Allee 11, D-89081 Ulm, FRG
 REMARK Revised by author 11-NOV-96

COMMENT On Nov 12, 1996 this sequence version replaced gi:1657351.
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BASE COUNT 364 a 402 c 354 g 455 t
ORIGIN

Alignment Scores:
Pident. No.: 4,55c-178 Length: 1575
Score: 1866.00 Matches: 358
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.72% Mismatches: 0
Query Match: 99.95% Indels: 0
DB: 10 Gaps: 0
US-09-367-052-2 (1-359) x MMLESTRPT (1-1575)

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QY 21 GlyAspTyRASPserAsnGluProCysPheArgAspGluAsnValHisPheAsnArg 40
DB 150 GGAGACTATGATCCCAAGAGAACCCGCTTCCGGATGAAAGCTCCATTTCATAGG 209
QY 41 IlePheLeuProThrIleTyRheIleIlePheLeuThrGlyIleValGlySncGlyLeu 60
DB 210 ATCTTCGCGCCACCATCTACTCTCATCTCTTGTGACGCGCATGTGGCATGATGATG 269
QY 61 ValIleLeuValMetGlyTyGlnIlySlyLeuArgSerMetThrAspIlyTyRgluLeu 80
DB 270 GTGATCCGTGATGATGGTTACCAAGAAAGCTAAGAGATGACGACAGTACCGGCTG 329
QY 81 HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheThrAlaValAspAla 100
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QY 121 AsnLeuTySerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyRLeuAlaIle 140
DB 450 AACCTCTACAGAGAGGTTCTCATCTGGCTTCATCAGCTGACCGGTGACTCCCTAT 509
QY 141 ValHisAlaThrAsnSerGlnArgProArgIlySlyLeuLeuAlaGluLysAlaValTyRVal 160
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QY 181 GlnGlyAspIleSerGlnGlyAspAspArgTyRileCysAspArgLeuTyRProAspSer 200
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QY 201 LeuTrpMetValValPheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIle 220
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DB 750 GTCATCTCTCTCTGTTACTGATCATCTCTATAGCTGTGTACACTCCAGAGGCCACAC 809
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DB 870 CCATATATATGTGGGATCAGATCAGATCCTTCATCTTTGGGGGCTCATCAACAGCA 929
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DB 990 CACTGTGCTCGAACCACCATCTCATATCTCTTCCGCGGCGCAAGTTCAAAAGCTCTGCC 1049
QY 321 GlnHisAlaLeuAsnSerMetSerArgIlySerSerLeuLysIleLeuSerIlyGlyLys 340
DB 1050 CAGCATGACACCACTCATGATGAGCAGAGCTCCACGCCCAAGATCTTCCAAAGAGAAAG 1109
QY 341 ArgGlyGlyHisSerSerValSerThrGluSerGluSerSerPheHisSerSer 359
DB 1110 CGGGGTGACACTCTCTCCGTCTCCAGGAGTCAAGATCTTCAGTTTCACTCCAGC 1166

RESULT 5
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LOCUS
DEFINITION Mouse mRNA for murine CXCR-4, complete cds.
ACCESSION AB000803
VERSION AB000803.1 GI:1816445
KEYWORDS murine CXCR-4; fusin.
SOURCE Mus musculus (strain: C57BL-6) E17 thymus cDNA to mRNA.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1809)
AUTHORS Suzuki, G., Nakata, Y., Uzawa, A., Shitasawa, T., Saito, T. and Mita, K.
TITLE Molecular cloning of murine CXCR-4, a murine homologue of HIV entry
co-receptor, that is expressed on leukocyte and other organs
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1809)
AUTHORS Suzuki, G.
TITLE Direct Submission
JOURNAL Submitted (29-JAN-1997) Gen Suzuki, National Institute of
Radiological Sciences, Division of Radiation Health; 4-9-1,
Anagawa, Inage-ku, Chiba, Chiba 263, Japan
(E-mail:gsuzuki@umx1.nirs.go.jp, Tel:043-251-2111,
Fax:043-284-1736)
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Alignment Scores:

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Score: 5.3e-178 Length: 1809  
Pred. No.: 1866.00 Matches: 358  
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US-09-367-052-2 (1-359) x AB000803 (1-1809)

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DB 132 GGAGACTATGACTCCAAACAGAAACCCGCTCCGGGATGAAACGTCATTTGCAATGAG 191  
OY 41 IlePheLeuProThrIleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeu 60  
DB 192 ATCTTCGCGCCACCATCTACTTCATCTTCATCTTCGATGCGCATAGTCGGAATGATGG 251  
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DB 252 GTGATCCGTCGTCATGCGTTACCAAGAAAGCTAAGACATCAGCGACAGTACCGGCTG 311  
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DB 312 CACCTGTCAGTGGCGGACCTCTCTTGTATCACAACCTCCCTCTCGCGAGTTGATGCC 371  
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LOCUS MLCR12 1180 bp mRNA linear ROD 18-NOV-1997  
DEFINITION Mus musculus lcr-1 gene.  
ACCESSION Z80112  
VERSION Z80112.1 GI:2632100  
KEYWORDS CXC chemokine receptor 4; CXCR-4; lcr-1 gene.  
SOURCE Mus musculus.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 1180)  
Schubel, A., Burstahler, R. and Lipp, M.  
The mouse homologue of the human HIV coreceptor CXCR-4 (FUSIN):  
High expression in thymus and lymphoid tissues  
unpublished  
2 (bases 1 to 1180)  
Lipp, M.  
Direct Submission  
Submitted (11-SEP-1996) Martin Lipp, Max-Deibnueck-Center for  
Molecular Medicine, MDC, Robert-Roessle-Strasse 10, BERLIN-BOCH,  
D-13122, GERMANY  
On Nov 21, 1997 this sequence version replaced gi:1542888.  
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Query Match: 98.98% Indels: 2
DB: 10 Gaps: 1

US-09-367-052-2 (1-359) x MMLCRL12 (1-1180)

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    61 ValIleLeuValMetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeu 80
    175 GTGATCCGCGTCATGGTTACCAGAAAGCTAAAGACATGACGACAGTACCGGCTG 234
    81 HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheThrAlaValAspAla 100
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    141 ValHisAlaThrAsnSerGlnArgProArgLysLeuAlaGluLysAlaValThrVal 160
    415 GTCCAGCGCCACCAAGTCAAAGGCCAAAGAACTGTGGCTGAAAGGACAGTATATG 474
    161 GlyValTyrPheProAlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSer 180
    475 GCGCGTGGATCCAGCCCTCTCTCTGACTATACCTGACTTCTTTGCCAGCTCAGC 534
    181 GlnGlyAspIleSerGlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSer 200
    535 CAGGGGAGCATCAGACAGGGGGATGACAGGTCACTGTGACCGGCTTACCCCATAGC 594
    201 LeuTyrMetValValPheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIle 220
    595 CGTGGATGGTGGTCTTTCATATCCAGCATATAAATGGGGCTCATCTCCGCCGCGATC 654
    221 ValIleLeuSerCysTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGln 240
    655 GTCACTCCTCTCTCTTACTGATCATCTCTTAAGCTGTGACATCCAGGCGCACAG 714
    241 LysArgLysAlaLeuLysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrLeu 260
    715 AAGCCCAAGGCCCTCAAGACGACACTCATCTCAGCTTCTTTGCCGTGGCTG 774
    261 ProTyrTyrValGlyIleSerIleAspSerPheIleLeuGlyValIleLysGlnGly 280
    775 CCATATATATGAGGATGACATGCACTCTTCATCTTTTGGAGTGCATCAAGACAGA 834
  
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QY 281 CysAspPheGluSerIleValHisLysTyrPheSerIleThrGlnAlaLeuAlaPhePhe 300
    TGTGACTTCGAGAGATTTGTGCACAGATGATCTTCATCAACAGAGGCCCTTCCTTC 894
    301 HisCysCysLeuAsnProIleLeuTyrAlaPheLeuGlyAlaValPheLysSerSerAla 320
    895 CACTGTTCCTGAGAACCCCATCTCTATGCTCTCTCCGGGGCCAAAGTCAAAAGCTTCGCC 954
    321 GlnHisAlaLeuAsnSerMetSerArgLysSerLeuLysIleLeuSerLysGlyLys 340
    955 CAGCTGGCACTCAATCATGACAGAGAGGCTCCAGCTCCAGATCTTTCCAAAGAGAAAG 1014
    341 ArgGlyGlyHisSerSerValSerThrGluSerGluSerSerSerPheHisSerSer 359
    1015 CGGGGTGACACTCTCTCCGCTCCAGCGGAGTCAAGATCTCTCATCTTCATCCAGC 1071

RESULT 7
MMLCRL3
LOCUS MMLCRL3 1422 bp DNA linear ROD 31-OCT-1996
DEFINITION Mus musculus lcr-1 gene, exon 2.
ACCESSION 280113
VERSION 280113.1 GI:1655638
KEYWORDS CXC chemokine receptor 4; CXCR-4; lcr-1 gene.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1422)
Schubel, A., Burgstahler, R. and Lipp, M.
The mouse homologue of the human HIV coreceptor CXCR-4 (FUSIN):
High expression in thymus and lymphoid tissues
Unpublished
2 (bases 1 to 1422)
Lipp, M.
Direct Submission
Submitted (11-SEP-1996) Martin Lipp, Max-Deiblbrueck-Center for
Molecular Medicine, MDC, Robert-Roessle-Strasse 10, BERLIN-BUCH,
D-13122, GERMANY
FEATURES
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location/Qualifiers
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    <1..259
    /number=1
    260..1422
    /gene="lcr-1"
    260..>1422
    /gene="lcr-1"
    /product="CXCR-4"
    /standard_name="CXC chemokine receptor 4"
    /number=2
    /function="receptor for chemokine SDF-1"

BASE COUNT 341 a 379 c 311 g 391 t
ORIGIN

Alignment Scores:
Pred. No.: 4.22e-175 Length: 1422
Score: 1836.00 Matches: 354
Percent Similarity: 99.44% Conservative: 2
Best Local Similarity: 98.88% Mismatches: 1
Query Match: 98.34% Indels: 1
DB: 10 Gaps: 0

US-09-367-052-2 (1-359) x MMLCRL13 (1-1422)

QY 3 ProIleSerValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAs 22
    244 CCGTGTCTCTTGGCAGATATACACTTCTGATTAATCTTCAAGAGAGTGGGCTGGAGA 303
    22 pTyrAspSerAsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePh 42
  
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Db      304 CTATAGCTCCAAAGAACCTGCTCCGGAGTAAACCTCATTTCAATAGATCTT 363
Oy      42 eleuProthrIleTyRPhelleIleIlePheLeuThrglyIleValaGlyasnGlyLeuValaI 62
Db      364 CCTGCCCAACCTCACTTCAATCATCTTCTTACGGCATATCGGCATATGATGGATGGATG 423
Oy      62 eleuValMetGlyTyRglnLysLysLeuArgSerMetThrSppLysTyRAlaGluHisLe 82
Db      424 CCTGCTATGGGTTACCAAGAAAGCTAAGAGATGACGACAAAGTACCGGCTGCACCT 483
Oy      82 uSerValAlaAspLeuLeuPheValIleThrLeuProPheTrpAlaValaAspAlaMetAl 102
Db      484 GTCAAGTGGCTGACCTCTCTTGTATCATCACACTCCCTTGTGGCAGATTGATGCATGGC 543
Oy      102 aAspTrpTyRPhelGlyLysPheLeuGlyLysAlaValaHisIleIleTyRThrValaHisLe 122
Db      544 TGACTGGTACTTGGGAAATTTTGTGTAGGGCTGTCCATATCATCACTGATCACT 603
Oy      122 uTySerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyRLeuAlaIleValaI 142
Db      604 CTACAGCAGCGCTTCTCATCTCGGCTTCAATCAGCTGACCGGTACCTCGGCATTTGTCCA 663
Oy      142 sAlaThrAsnSerGlnArgProArgLysLeuLeuAlaGlyLysAlaValaTyRValaGlyVa 162
Db      664 CGCCACCAACAGTCAAGAGCCCAAGAAACTGCTGCTGAAAGCAGTCTATGTGGCGCT 723
Oy      162 lTrpIleProAlaLeuIleLeuThrIleProAspPheIlePheAlaAspValaSerGln 182
Db      724 CTGGATCCACCGCTCTCTCTGCTATACCTGACTTCACTTCTCCGCGCTACCGCAGG 783
Oy      182 yAspIleSerGlnLysAspAspArgTyRLeuAspArgLeuTyRProAspSerLeuTr 202
Db      784 GGACATCATGTCAGAGGGATGACAGGTATCATCTGTAGCCGCTTTACCCGATACCGCTGTG 843
Oy      202 pMetValaIlePheGlnPheGlnHisIleMetValaGlyLeuIleLeuProGlyIleValaI 222
Db      844 GATGGTGTGTTCATATCCAGCATATATGATGGTGTCTATCTCTGCCCGGCATCGTCAT 903
Oy      222 eleuSerCysTyRcysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysAr 242
Db      904 CCTCTCCGTATGATGATCATCATCTCTAGCTGTACACTGCACAAAGGCGCACAGAAAGCG 963
Oy      242 gLysAlaLeuLysThrThrValaIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTy 262
Db      964 CAAGGCCCTCAAGAGCAGATCATCTCATCTTCTTGGCTGCTGCTGCCATTA 1023
Oy      262 rTyRValaGlyLysSerIleAspSerPheIleLeuLeuGlyValaIleLysGlnGlyCysAs 282
Db      1024 TTATGTGGGGATCGACATCGACTCTCTCATCTTTTGGAGTCAATCAAGCAAGAGATGTA 1083
Oy      282 pPheGluSerIleValaHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCys 302
Db      1084 CTTGAGAGCATTTGTGCACAAAGTGAATCTCCATCAACAGAGCCCTCGCTTCTTCCACTG 1143
Oy      302 sCysLeuAsnProIleLeuTyRAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnH 322
Db      1144 TTGCCTGAACCCCATCTCTATGCTTCTCTCGGGGCCAAAGTTCAAAAGCTTGTGCCACGA 1203
Oy      322 sAlaLeuAsnSerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgG 342
Db      1204 TGCACTCAACATCCATGACAGAGGCTCCAGCCTCAAGATCCTTTCCAAAGCAAGCGGG 1263
Oy      342 yGlyHisSerSerValSerThrGluSerGluSerSerSerPheHisSerSer 359
Db      1264 TGGACACTTTCCTCGCTCCAGAGTCAAGAAATCTCCAGTTTCACTTCACG 1315

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KEYWORDS

SOURCE

Mus musculus.
Mus musculus.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognath; Muridae; Mus.

REFERENCE

1 (bases 1 to 3366)
Heesen,M., Berman,M.A., Benson,J.D., Gerard,C. and Dorf,M.E.

AUTHORS

Cloning of the mouse fusin gene, homologous to a human HIV-1
co-factor

TITLE

J. Immunol. 157 (12), 5455-5460 (1996)

JOURNAL

97113334

MEDLINE

8955194

PUBMED

2 (bases 1 to 3366)

REFERENCE

Heesen,M., Berman,M.A., Gerard,C. and Dorf,M.E.

AUTHORS

Direct Submission

TITLE

Submitted (30-JUL-1996) Pathology, Harvard Medical School, 200
Longwood Avenue, Boston, MA 02115, USA

JOURNAL

Location/Qualifiers

FEATURES

source

gene

1..3366

CDS

join(1..21,2308..3366)

exon

1..21

intron

22..2307

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2308..3366

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intron

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exon

3367..3366

intron

3367..3366

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DEFINITION Mus musculus fusin (CXCR-4) gene, complete cds.
ACCESSION  U65580
VERSION     U65580.1  GI:1731650

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QY      42  eleuProthrIleTyrPheIleIlePheleuThrglyIleValGlyAsnGlyLeuValI1 62
      |||
      2412 CCGGCCACCATGCTACTTCAATCTCTTGACGCGATGTCGGCAATGATGGATGAT 2471

Db      62  eleuValMetGlyTyrGlnIlySlyLeuAArgSerMetThrAspLysTyrArgLeuHisLe 82
      |||
      2472 CCGGGTCATCGGTTTACAGAGAGAGCTAAGAGCATACAGACAGTACAGTACCGCGCTGCACT 2531

QY      82  uSerValAlaAspLeuLeuPheValIleThrIleuProPheThrAlaValAspAlaMetAl 102
      |||
      2532 GTCAATGGCTGACCTCTCTTGTGATCAACACTCCCTTGCGGCACTTATGCGCATGGC 2591

Db      102 aasPTTPTyrPheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLe 122
      |||
      2592 TGACTGCTACTTTGGGAAATTTTGTGTAAAGCGCTGCATATCATCTACACTGTCACACT 2651

QY      122 uTyrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValH1 142
      |||
      2652 CTACAGCAGCGGTTCTCTCTGCGCTTCATCAGCGCTGACCGGATCTCCCATTTGTCCA 2711

Db      142 sAlaThrAsnSerGlnArgProArgLysLeuLeuAlaGlyLysAlaValAlaTyrValGlyA 162
      |||
      2712 CGCCACCACAGTCATAAGGCCAAGAGAACTGTGGCTGAAGAGGCACTATGTGGGCGT 2771

QY      162 lTrpIleProAlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnG1 182
      |||
      2772 CTGGATCCCAAGCCCTCTCTGACTATACCTGACTTCTTCCCGACGTCACAGCCAGGG 2831

Db      182 yAspIleSerGlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuT 202
      |||
      2832 GGACATCATGTCAGGGGATGACAGGTACATCTGTGACCGGCTTACCCCATGACCTGTG 2891

QY      202 pMetValValPheGlnPheGlnHisIleMetValGlyLeuIleuProGlyIleValI1 222
      |||
      2892 GATGGTGGTGTTCATTCACAGCATATATGATGGTGTCTATCTGCGGCGATCGTCAT 2951

Db      222 eleuSerCysTyrCysIleIleIleSerLysLysSerHisSerLysGlyHisGlnLysAr 242
      |||
      2952 CCTCTCTGTATACGATCATCATCATCAAGCTGTCACTCCCAAGGCCACCGAAGCG 3011

QY      242 gLySAlaLeuLysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrLeuProTy 262
      |||
      3012 CAAGGCCCTCAAGCAGACATCATCTCATCTGCTTCTTCTGCTGCTGCGCATG 3071

Db      262 rTyrValGlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAs 282
      |||
      3072 TTATGTGGGATGATGATCATCTCTTCATCTTTTGGGGGTCTATCAAGCAAGGATGTGA 3131

QY      282 pPheGlnSerIleValHisLysTyrPheIleThrGlnAlaLeuAlaPhePheHisCys 302
      |||
      3132 CTTCGAGAGCATCTGTCACAAAGTGATCTCATACAGAGGCCCTCCCTTCTTCCACTG 3191

Db      302 sCysLeuAsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnH1 322
      |||
      3192 TTGGCTGAAACCCCTCTATGCTTCTCTGCGGGGCAAGTCAAAAGCTCTGCCAGCA 3251

QY      322 sAlaLeuAsnSerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgG1 342
      |||
      3252 TGCACTCACTCCATGAGCAGAGGCTCAGCTCAAAATCTTCCCAAGAAAGCGGGG 3311

Db      342 yGlyHisSerSerValSerThrGlnSerGlnSerSerPheHisSerSer 359
      |||
      3312 TGGACACTCTTCGCTCTCCAGGAGTCAAGATCTCTCAGTTTTCATCTCCAGC 3363

RESULT 9
MMLESTRGN 3770 bp DNA linear ROD 02-APR-1997
LOCUS M_musculus gene encoding leukocyte-derived seven transmembrane
DEFINITION domain receptor, strain B6.
ACCESSION X9581
VERSION X9581.1 GI:1924959
KEYWORDS lestr gene; leukocyte-derived seven transmembrane domain receptor.

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SOURCE Mus musculus.
ORGANISM Mus musculus
Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Rodentia; Sclerognathia; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 3770)
AUTHORS Moepks,B., Frodl,R., Kessler,H. and Gierschik,P.
TITLE cDNA cloning and genomic organization of a leukocyte-derived seven
transmembrane domain receptor (LESTR) from mouse: a murine
homologue of the human HIV-1 entry cofactor fusin
JOURNAL unpublished
REFERENCE 2 (bases 1 to 3770)
AUTHORS Moepks,B.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-1996) B. Moepks, Universitaet Ulm,
Pharmacology/Toxicology, Albert-Einstein Allee 11, D-89081 Ulm, FRG
REMARK Revised by [3]
REFERENCE 3 (bases 1 to 3770)
AUTHORS Moepks,B.
TITLE Direct Submission
JOURNAL Submitted (02-APR-1997) B. Moepks, Universitaet Ulm,
Pharmacology/Toxicology, Albert-Einstein Allee 11, D-89081 Ulm, FRG
COMMENT On Apr 3, 1997 this sequence version replaced gi:166646.
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/db_xref="SWISS-PROT:P70658"
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GVWLPALLTIPDTFADVSQDISQDDRYICDRIYPSDLMWVFOFHITWGLVLP
GIYLSCYCIILIKLSHKGQRKALKATVILIAFFACMLPYVVGISIDSRLLIGV
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BASE COUNT 824 a 934 c 947 g 1065 t
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Pred. No.: 1,56e-174 Length: 3770
Score: 1835.00 Matches: 353
Percent Similarity: 99.44% Conservative: 3
Best Local Similarity: 98.60% Mismatches: 1
Query Match: 98.29% Indels: 1
DB: 10 Gaps: 0
US-09-367-052-2 (1-359) x MMLESTRGN (1-3770)
QY 3 Proileser-ValserIleTyrThrSerAspAsnTyrSerGlnGluValGlySerGlyAs 22

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Db      2290 CCTGTTCTTCCTTGGAGATATACACTTCTGATACTCTGAGAAAGTGGTCTTGAGA 2349
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Db      2350 CTATGACTCCAAACAGAACCCCTGCTCCGGGATGAAACGCTCATTTCAATAGAGACTT 2409
Qy      42  eLeuProThrIleTyrrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuVal11 62
Db      2410 CTTGCCACCATCTACTTTCATCTTCTTGACTGGCATAGTGGCATGATGGTGTGAT 2469
Qy      62  eLeuValMetGlyTyrrGlnLysLysLeuArgSerMetThrAspLysTyrrArgLeuHis1e 82
Db      2470 CTTGCTGATGGGTATACAGAAAGCTAAGAGCATGACGACAGTACCGCGCTGACCT 2529
Qy      82  uSerValAlaAspLeuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAl 102
Db      2530 GTCACTGGTGGACCTCTCTTTGTCATCACACCTCCCTTGCGCACTTATGATGACATG 2589
Qy      102  aAspTrpTyrrPheGlyLysPheLeuCysLysAlaValHisIleIleTyrrThrValAsn1e 122
Db      2590 TGACTGTTACTTGGGAAATTTTGTATAGGCTGTCTCATATCATCTACCTGTCAACT 2649
Qy      122  uTyrrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrrLeuAlaIleVal1H 142
Db      2650 CTACAGCAGCGCTTCTCATCTCGGCTTCATCAGCGCTGACCGTACCTCGCTATGTGCA 2709
Qy      142  sAlaThrAsnSerGlnArgProArgLysLeuLeuAlaGlyLysAlaValTyrrValGlyVa 162
Db      2710 CGGCACCAACAGTCAGAGCCCAAGAAAGTGTGGCTGGAAGAGCACTATGTTGGCGCT 2769
Qy      162  lTrpIleProAlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGln1 182
Db      2770 CTGATGCCAGCCCTCTCTGACTATACCTGACTTATCTTGGCCACTGACCGCAGG 2829
Qy      182  yAspIleSerGlnGlyAspAspArgTyrrIleCysAspArgLeuTyrrProAspSerLeuTr 202
Db      2830 GGCATCATAGTCAGGGGATACAGGTACATCTGTGACCGCGCTTACCCCGATAGCCGTG 2889
Qy      202  pMetValValPheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleVal11 222
Db      2890 GATGGTGCTTTTCAATTCACGATATATAGTGGTGTCTGCTGCGCGGCAATCGCAT 2949
Qy      222  eLeuSerCysTyrrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysAr 242
Db      2950 CCTGCTCTGTACTGATCATCATCTCTAGCTGTACACTCCAAAGGCCACCAAGAGCG 3009
Qy      242  glyValAlaLeuLysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTy 262
Db      3010 CAAGGCCCTCAACAGCACATCATCTCATCTGCTTCTTGGCTGCGCTGCCATTA 3069
Qy      262  rTyrrValGlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAs 282
Db      3070 TTTATGCGGATATACGATTCACATCTCTTATCTCTTGGGGGTATCAAGAAAGATGTGA 3129
Qy      282  pPheGluSerIleValHisLysTrpIleSerIleThrGlyAlaLeuAlaPhePheHisCys 302
Db      3130 CTTGAGAGAGCATGTGACAAAGTGAAGTCTCATCACAGAGCGCTGCTTCTTCCACTG 3189
Qy      302  sCysLeuAsnProIleLeuTyrrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnH 322
Db      3190 TTTCCCTGAACCCCATCTCTATGCTCTCTCCGCGGCAAGTTCAAAAGCTCTCCACGA 3249
Qy      322  sAlaLeuAsnSerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgG1 342
Db      3250 TGGACTCAACTTCATAGAGAGAGGCTCCACCTCAAGATCTTTCCAAAGAAAGCGGG 3509
Qy      342  yGlyHisSerSerValSerThrGluSerGluSerSerSerPheHisSerSer 359
Db      3310 TGGACACTCTTCGCTCTCCAGGAGTCAAGATCTCTCAGTTTCACTCCAGC 3361

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RESULT 10
AF452185

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LOCUS      AF452185                1050 bp    mRNA       linear   ROD 18-DEC-2001
DEFINITION Rattus norvegicus strain Holtzman chemokine receptor CXCR4 (CxCr4)
ACCESSION  AF452185
VERSION    AF452185
KEYWORDS
SOURCE     Rattus norvegicus.
ORGANISM   Rattus norvegicus.
REFERENCE  1 (bases 1 to 1050)
AUTHORS   Simen,A.A. and Miller,R.J.
TITLE      Chemokine regulation of neuronal signaling and gp120 neurotoxicity
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 1050)
AUTHORS   Simen,A.A. and Miller,R.J.
TITLE      Direct Submission
JOURNAL    Submitted (25-NOV-2001) Dept. Psychiatry, Yale University, New
           Haven, CT 06508, USA
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                        /strain="Holtzman"
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                        /sex="female"
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                        1..1050
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                        /db_xref="GI:17902281"
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           /translacion="MEIYSDNYSEREGSGDYDSNKEPCRDENENFNRIPLTYFI
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           ALLRTIPDIIPADVSGDGRYICDRLYPSLIMVYVPOFOHIVGILIPITVILSCYI
           IISKISHSGHCKRRLKLTIVTILITLAFRCWLPYVYGISIDFTLILEVYKOCPEFV
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Score:          1758.50      Matches:      340
Percent Similarity: 97.18%      Conservative: 4
Best Local Similarity: 96.05%      Mismatches: 5
Query Match:    94.19%      Indels:      5
DB:              10      Gaps:      1
US-09-367-052-2 (1-359) x AF452185 (1-1050)
Qy      6  valSerIleTyrrThSerAspAsnTyrrSerGluGluValGlySerGlyAspTyrrAspSer 25
Db      1  ATGGAATATATACACTTCCGATAACTATCTCCGAAGAGTGGGTCTGGAGACTATGACTCC 60
Qy      26  AsnLysGluProcysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db      61  AACAAAGAACCCGCTTCCGGGATGAAACGAAAACTTCAACAGATCTTCTGCCACAC 120
Qy      46  lIleTyrrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db      121  ATCTATTTTATATCATCTTCTTGACTGGCATAGGAGGCTGTGTAATCTCTGGTCATG 180
Qy      66  gLTYrGlnLysLysLeuArgSerMetThrArgLysLysTyrrArgLeuHisLeuSerValAla 85

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Db      181 GGTACCAGAGAGCTGAGAGCATGACAGACAACTACCGGCTGACCTGCTCGTGGCT 240
Oy      86 AspleuDeupheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTrpTyr 105
Db      241 GACCTCTCTTTTGTTCATCACACATCCCTCTTGCGGACATGAGCGCATGGCTGATGCTGATC 300
Oy      106 PheGlyLysPheLeuCysLysAlaValAlaHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db      301 TTGGGAAATTTTATATTAAGGCTGTGCATATATCTACACCGCTCAACCTTTTACAGCAGT 360
Oy      126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db      361 GTTCTCATCTGGGCTTCATCAGCTGACCGGCTGACCTGCAATTTGCCAGCCACCAAC 420
Oy      146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValAlaTrpIlePro 165
Db      421 AGCCAGAGAGCGGAGAGAGCTGCTGGCTGAAGAGCGCTCATGTGGGTGCTGGATCC 480
Oy      166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db      481 GCCCTCTCTCGATATCCCGACATCATCTTCCGCGATGTC-----AGC 525
Oy      186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
Db      526 CAGGGGAGCGGAGAGCTACATCTGTGACCGCTTACCAGCCAGACCTGTGGATGGTGGT 585
Oy      206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db      586 TTCAGTTCACGACATCATGTGGGTGCTCATCTCGCGGACATCGTATCTGCTGCT 645
Oy      226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlnHisGlnLysArgLysAlaLeu 245
Db      646 TACGTCATCATCATCTCCAGCTGTCTACACTCCAGAGGCCACGAAAGCCGACGCCCTC 705
Oy      246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
Db      706 AAGCTACAGGTCATCTTATCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 765
Oy      266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db      766 ATCGCATCATCTCTCATCTCTTGTGAGGTCTCATCAAGAGCTCCGCGCAGCATGCACAT 825
Oy      286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db      826 GTGCTGACAAAGTGCATCTCATACGAGAGGCCCTCCCTTCTTCCACTGTGCTGCTAAC 885
Oy      306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db      886 CCCATCTCTACGCTTCTCTCGGGGCAAAATTCAAAGAGCTCCGCGCAGCATGCACAT 945
Oy      326 SerSerSerArgGlySerSerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
Db      946 TCATGTGACAGAGGCTCCAGCTCAAGATCTTTCCAAAGGGAACCGGGGTGACACTCT 1005
Oy      346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
Db      1006 TCCGCTCTCCAGAGGTGAGATCTCTCAAGTTTTCACCTCCAGC 1047

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RESULT 11
RNU90610      1050 bp mRNA linear ROD 26-MAR-1997
LOCUS         Rattus norvegicus CXc chemokine receptor (CXCR4) mRNA, complete
DEFINITION   cds.
ACCESSION    U90610
VERSION      U90610.1 GI:1906612
KEYWORDS     Rattus norvegicus.
SOURCE       Rattus norvegicus.
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
              Rattus.
REFERENCE    1 (bases 1 to 1050)

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AUTHORS      Harrison, J.K. and Salafraanca, M.N.
TITLE        Molecular cloning of rat CXCR4
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 1050)
AUTHORS      Harrison, J.K. and Salafraanca, M.N.
TITLE        Direct Submission
JOURNAL      Submitted (25-FEB-1997) Pharmacology and Therapeutics, University
              of Florida, 1600 SW Archer Rd., Gainesville, FL 32610-0267, USA

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    ALLITPDILEADVDSQDGRYICDRLYDPSLMMVWFQFQIHMGILIPGVITISCYCI
    TISKLSKSKHOKRKALKTYVILILAFACMEYRYVIGISIDSTILEVIRKQCFESV
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BASE COUNT   231 a      313 c      247 g      259 t
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Alignment Scores:
Pred. No.:    4.77e-166      Length:    1050
Score:        1744.50        Matches:    338
Percent Similarity: 96.61%      Conservative: 4
Best local Similarity: 95.48%      Mismatches: 7
Query Match:  93.44%          Indels:    5
DB:            10            Gaps:    1

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Oy      6 ValSerIleTyrThrThrAspAspArgTyrSerGluGluValGlySerGlyAspTyrAspSer 25
Db      1 ATGGAAATATACATCTTGATGATACCTCGAAGAAATAGGCTGAGACTATGACTCC 60
Oy      26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db      61 AACAGAGAACCCGCTCCGGGATGAAAGAAACTTCAACAGAGATCTTCCGCCAC 120
Oy      46 IleTyrPheIleIlePheLeuThrGlyIleValGlyLysGlnGlyLeuValIleLeuValMet 65
Db      121 ATCTATTTTATCATCTTCTTGACGCGCATGTGGGCAATGGGTGGTAACTCTGCTCATG 180
Oy      66 GltTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db      181 GGTACCAGAGAGAGCTGAGAGCATACACAGACAGTACCGGCTGACCTGTCCGTGGCT 240
Oy      86 AspleuDeupheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTrpTyr 105
Db      241 GACCTCTCTTTTGTTCATCACACATCCCTCTTGCGGACATGAGCGCATGGCTGATGCTGATC 300
Oy      106 PheGlyLysPheLeuCysLysAlaValAlaHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db      301 TTGGGAAATTTTATATTAAGGCTGTGCATATATCTACACCGCTCAACCTTTTACAGCAGT 360
Oy      126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db      361 GTTCTCATCTGGGCTTCATCAGCTGACCGGCTGACCTGCAATTTGCCAGCCACCAAC 420
Oy      146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValAlaTrpIlePro 165

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Db      481 GCCCTCCTCCGACTATCCGACATCATCTTCCCATGTC-----AGC 525
Qy      186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProaspSerLeuTyrMetValVal 205
Db      526 CAGGGGAGGAGGAGAGTACATCTGTGACCGCTTACCAGCCAGACCTGTGATGTGTG 585
Qy      206 PheGlnPheGlnHisIleMetValGlyLeuLeuProGlyIleValIleLeuSerCys 225
Db      586 TTCACGATTCACGACATCATCTGTGCTCTCTCCGCGGACATCATCTGCTCTGT 645
Qy      226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db      646 TACGTCATCATCTCTCCAGCTTCACACTCCAGAGGCCACCAAGCCAGAGGCCCTC 705
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Db      706 AAGACTAGGTCATCTTATCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
Qy      266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db      766 ATCAGCATCATCTCTCATCTCTTGTGAGTCTATCAAGAGCATGTGATTCGAGAGC 825
Qy      286 IleValHisLysThrPheIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db      826 GTGCTGCACAGTGTGATCTCCATCAGGAGGCCCTCCCTCTTCCATGTTGCTGCTAAC 885
Qy      306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db      886 CCCATCTCTACGCTTCTCTGCGGGCCAAATCAAGAGCTCCGCGGACATGCTCAT 945
Qy      326 SerIleSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyHisSer 345
Db      946 TCCATGTGACAGAGGCTCAGGCTCAAGATCTTTCACAAAGGAGGAGGAGGAGCT 1005
Qy      346 SerValSerThrGlnSerGluSerSerSerPheHisSerSer 359
Db      1006 TCCGTCCTCCACAGAGTCAGATCTCTCAAGTTTTCACCTCCAGC 1047

RESULT 12
AF031089 1059 bp mRNA linear PRI 14-OCT-1998
LOCUS Papio hamadryas anubis CXc chemokine receptor 4 (CXCR4) mRNA,
DEFINITION complete cds.
ACCESSION AF031089
VERSION AF031089.1 GI:2625093
SOURCE
ORGANISM Papio cynocephalus anubis.
          Papio cynocephalus anubis
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
          Cercopithecinae; Papio.
REFERENCE
  1 (bases 1 to 1059)
  Benton, P.A., Lee, D.R. and Kennedy, R.C.
  Sequence comparisons of non-human primate HIV-1 coreceptor
  homologues
  Mol. Immunol. 35 (2), 95-101 (1998)
JOURNAL
  MEDLINE
  98346785
  2 (bases 1 to 1059)
  Benton, P.A. and Kennedy, R.C.
  Direct Submission
  Submitted (22-OCT-1997) Microbiology and Immunology, University of
  Oklahoma Health Sciences Center, 800 Research Parkway, Rm 458,
  Oklahoma City, OK 73104, USA
  Location/Qualifiers
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FEATURES
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QY 246 LysThrThrValIleLeuIleLeuAlaIlePhePheAlaCysTrpLeuProTyrTyrValGly 265
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QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerAlaGlnHisAlaLeuAsn 325
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Db 895 CCCATCCCTATGCTTCTTCTTGAGCCAAATTAACCTCTGCCAGCAGCAGCTCACCC 954
QY 326 SerMetSerArgLysSerSerLeuLyslleLeuSerLysGlyLysArgGlyLysHisSer 345
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Db 955 TCTGTGACGACAGGCTCCAGCTCAAGATCTCTCTCCAAAGAAAGCGAGGCGACATTCCG 1014
QY 346 SerValSerThrGlnSerGlnSerSerSerPheHisSerSer 359
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Db 1015 TCTGTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCAGC 1056
RESULT 13
AF001928 1087 bp mRNA linear PRI 10-MAR-1998
LOCUS Macaca mulatta alpha-chemokine receptor 4 (CXCR4) mRNA, complete cds.
DEFINITION
ACCESSION AF001928
VERSION AF001928.1 GI:2911293
KEYWORDS
SOURCE Macaca mulatta.
ORGANISM Macaca mulatta.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopitheciinae; Macaca.
REFERENCE
AUTHORS Pretel,J.-L., Guillet,J.-G. and Butor,C.
TITLE New widespread CXCR4 allele in rhesus macaques does not predict
subspecies or clinical evolution
JOURNAL AIDS Res. Hum. Retroviruses 14 (7), 639-641 (1998)
MEDLINE 98252393
PUBMED 9591719
2 (bases 1 to 1087)
REFERENCE Pretel,J.-L., Guillet,J.-G. and Butor,C.
AUTHORS Direct Submission
TITLE Submitted (01-MAY-1997) INSERM U445, ICGM, 22 rue Mechain, Paris
JOURNAL 75014, France
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Query Match: 90.17% Indels: 5
Gaps: 1
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QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 98 ATTAAGGACCCCTGCTTCCGAGAGAAATGCTCATTTTCATAGATCTTCTCCACACC 157
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QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgGlnLeuHisLeuSerValAla 85
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Db 278 GACCTTCTCTTGTTCATACAGCTTCCCTTGGGAGATGATGCGCGTGGCAACTGCTAC 337
QY 106 PheGlyLysPheLeuCysLysAlaValHisIlelleTyrThrValAsnLeuTyrSerSer 125
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Db 518 GCCCTCCGCTGACTATTCGCCGACTCATCTTGGCCACCGTC -----AGT 562
QY 186 GlnGlyAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValAla 205
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QY	326	SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer	345	
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LOCUS	AB015943	1068 bp	mRNA	linear PRI 06-FEB-1999
DEFINITION	Chlorocebus aethiops mRNA for CXCR4 receptor, complete cds.			
ACCESSION	AB015943			
VERSION	AB015943.1	GI:3294341		
ORIGIN	CXCR4 receptor.			
ORIGIN	Chlorocebus aethiops cDNA to mRNA.			
ORIGIN	Euryarchaea: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:			
ORIGIN	Mammalia: Eutheria: Primates: Catarrhini: Cercopithecoidea:			
ORIGIN	Cercopithecoidea: Cercopithecus.			
ORIGIN	1 (bases 1 to 1068)			
ORIGIN	Murayama,Y., Matsunaga,S. and Inoue-Murayama,M.			
ORIGIN	cDNA sequence of African green monkey CXCR-4 chemokine receptor			
ORIGIN	gene			
ORIGIN	Published Only in Database (1998)			
ORIGIN	2 (bases 1 to 1068)			
ORIGIN	Murayama,Y., Matsunaga,S. and Inoue-Murayama,M.			
ORIGIN	Direct Submission			
ORIGIN	Submitted (01-JUL-1998) Yutchi Murayama, National Institute of			
ORIGIN	Animal Health, Food Safety Research Laboratory, Kanondai 3-1-1,			
ORIGIN	Tsukuba, Ibaraki 305-0856, Japan (E-mail: mspockebc.mhn.or.jp,			
ORIGIN	Tel: +81-298-38-7840, Fax: +81-298-38-7825)			
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ORIGIN	YFGEFLCKAHVITVNDVYSSVLLAFISDRYAIYHATNSQRPRLAEKVYGVSV			
ORIGIN	WIPLLLTLPHFIFASVEDDRYICRFEPNDLVVYFQOHIMVGLIPGIVILSC			
ORIGIN	YCIILSLSHSGHQRKRAKTYTILIAFAFWLPYIGISIDSLFLEIKGCEFEF			
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ORIGIN	ORIGIN			
ORIGIN	Alignment Scores:			
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ORIGIN	Best Local Similarity: 90.40%	Mismatches: 13		
ORIGIN	Query Match: 89.96%	Indels: 5		
ORIGIN	DB: 9	Gaps: 1		
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ORIGIN	Db	10	ATCAGTATATACACTTTCAGATTAACACCGAGAAATGGGCTCAGGGGACTATAGATCC	69
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Db	190	GGTTACCAAGAAACAGAGAGATGACGGACAGTACAGCGTCACCTTCAGTGGCT	249
Qy	86	AspLeuPhePheValIleThrLeuProPheArgPheValAlaAspAlaMetValAspTrpTyr	105
Db	250	GACCTCTCTTTGTTCATCACGCTTCCCTTCCTGGCAGTTGATGCCGTGGCAACTGGTAC	309
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Db	310	TTTGGGAAGCTCTGTGGGAAGGAGCTGCATGTATCTACAGAGTCAACCTTACAGCAGT	369
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Qy	266	IleSerIleAspSerPheIleLeuGlyValIleLysGlnGlyCysAspPheGlnSer	285
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Db	835	ACTGTGCACAAGTGGATTTCCATCATCAGGAGGCCCTTATTTTCCACTGTGTGTCAAC	894
Qy	306	ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn	325
Db	895	CCCATCTCTATGCTTCTTCTGTGAGCCCAAAATTTTAAACCTCTGCCAGCAGCACTCAC	954
Qy	326	SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer	345
Db	955	TCTGTGACGAGAGGGTCCAGCTCAAAATCTCTCCAAAGAAAGCAGAGGGGCACTCG	1014
Qy	346	SerValSerThrGlnSerGlnSerSerSerPheHisSerSer	359
Db	1015	TCTGTTCACACTGAGCTGTGAGTCTTCAAGATTTCACCTCCACC	1056
RESULT 15			
LOCUS	D86579	1078 bp	mRNA linear PRI 07-FEB-1999
DEFINITION	Macaca fascicularis mRNA for fusin (LESTR), complete cds.		
VERSION	D86579.1	GI:1468948	

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 15:58:43 ; Search time 207 Seconds
(without alignments) 3905.640 Million cell updates/sec

Title: US-09-367-052-2
Sequence: 1867
1 MEPISTVITRSDNSEEVS.....KRGSHSVTSRESSSFHSS 359

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+g2n.model -DEV=xlh
-O=/cgn2.1/USPRO.spool/US09367052/unat_10072003_100043_10328/app_query.fasta_1.519
-DB=N.Geneseq_101002 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum2 -TRANS=human40.cdf
-LIST=45 -DOCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09367052_ECGN_1.1_200_etunat_10072003_100043_10328 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESOURT -NEG SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N.Geneseq_101002:*

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- 14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
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- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1867	100.0	1758	20	AA227611
2	1867	100.0	1877	19	AAV46370
3	1678.5	89.9	1059	21	AA238553
4	1678.5	89.9	1059	24	AAH99952
5	1678.5	89.9	1588	20	AA227610
6	1678.5	89.9	1664	21	AAA61656
7	1678.5	89.9	1664	21	AA240014
8	1678.5	89.9	1670	24	ABK83803
9	1678.5	89.9	1670	24	ABN95645
10	1678.5	89.9	1679	22	AA165457
11	1678.5	89.9	1679	22	AAAD12801
12	1678.5	89.9	1737	16	AAO80521
13	1678.5	89.9	1737	16	AAO99007
14	1672.5	89.6	1059	23	AB197982
15	1672.5	89.6	1317	19	AAV18357
16	1672.5	89.6	1317	21	AAV1726
17	1672.5	89.6	1317	24	ABK54255
18	1672.5	89.6	1944	20	AA15882
19	1672.5	89.6	5161	21	AA20886
20	1672.5	89.6	5161	21	AAA34774
21	1672.5	89.6	5161	21	AAH99551
22	1667.5	89.3	1737	13	AAO29506
23	1662.5	89.0	1317	15	AAO66179
24	1658.5	88.8	1119	24	AAK98241
25	815	43.7	606	24	ABA92962
26	584	31.3	1107	21	AAA30593
27	584	31.3	1159	20	AA232713
28	584	31.3	1670	19	AAV26557
29	584	31.3	1670	24	ABN97338
30	581.5	31.1	1620	19	AAV43793
31	580	31.1	1107	21	AAA30714
32	575	30.8	1876	18	AAH72800
33	575	30.8	1877	22	AAH35033
34	570.5	30.6	1327	22	ABA09210
35	570.5	30.6	1677	17	AAA58872
36	567.5	30.4	1607	21	AA135277
37	555	29.7	1068	24	ABK16598
38	552	29.6	1068	24	ABK16599
39	551.5	29.5	1200	13	AAO30011
40	551.5	29.5	1200	16	AAO99949
41	550.5	29.5	1106	16	AAO99952
42	550.5	29.5	2072	24	AA517156
43	550.5	29.5	2084	24	ABK54274
44	550.5	29.5	2085	21	AA51745
45	549.5	29.4	1068	24	ABK16592

ALIGNMENTS

RESULT 1
ID AA227611 standard; DNA: 1758 BP.

AC AA227611;
XX
XX 16-DEC-1999 (first entry)
DT
XX Mouse CXCR4 coding sequence.
DE
XX
XX CXCR4: mouse; neovascularisation; inhibitor; solid cancer; therapy;
KW tissue repairing agent; vascularisation; ss.
XX
XX Mus sp.
OS

PN WO9948528-A1.
XX
XX 30-SEP-1999.
PD

XX
DR WPI: 1998-447232/38.
DR P-PSDB: AAW64778.
XX
PT Mouse CXK chemokine receptor binding to PBSF/SDF-1 pre-B cell
PT stimulatory factor - is useful for screening of potential HIV
PT infection and AIDS inhibitors
XX
HS Claim 3: Pages 39-42; 76pp; Japanese.
XX
CC The present sequence encodes a murine CXK chemokine receptor which
CC binds to the mouse CXK chemokine pre-B cell stimulatory factor
CC PBSF/SDF-1. The nucleic acid is isolated from mouse pre-B cell
CC line DW34. The receptor and cells expressing it can be used in the
CC study and mapping of the mechanism of HIV infection and in screening
CC of potential inhibitors of HIV infection and the development of AIDS.
XX
SQ Sequence 1877 BP; 469 A; 451 C; 406 G; 551 T; 0 other;

Alignment Scores:
Query: 2.8e-209 Length: 1877
1867.00 Matches: 359
Percent Similarity: 100.008 Conservative: 0
Best Local Similarity: 100.008 Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-367-052-2 (1-359) x AAW6370 (1-1877)
QY 1 MetGluProIleSerValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySer 20.
DB 120 ATGGACCGCATGAGTGAATATACACTTGATTAACACTGAGCAAGTGGGCT 179
QY 21 GLASPTyrSerSerAsnGluProGlyPheArgAspGluValHisPheAsnArg 40
DB 180 GGGAGCTAGTACATCCAAAGAACCTGCTCCGGGATGAAACGTCATTCAATAGG 239
QY 41 IlePheLeuProThrIleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeu 60
DB 240 ATCTCTCTGCCACATCTCTCTCATCATCTCTTGTGCTGGCATAGCGGCATGGATTG 239
QY 61 ValIleLeuValMetGlyTyrGlnGlyLysLeuArgSerMetThrAspLysTyrArgLeu 80
DB 300 GTATCTCTGCTCATGGTTCACAGAACCTTAAGAGCATGACGACAGTACCGGCTG 359
QY 81 HisLeuSerValAlaAspLeuPheValIleThrLeuProThrPheAlaValAspAla 100
DB 360 CACCTGTCACTGCTGACCTCTCTTGTGTCATCACACTCCCTTCTGGCAGTTGATGCC 419
QY 101 MetAlaAspTyrPyrPheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrVal 120
DB 420 ATGGCTAGCTAGTACTTTGGGAAATTTTGTGTAAGCTTCCATATCATCTACACTGTC 479
QY 121 AsnLeuTyrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIle 140
DB 480 AACCTCTACAGCAGCGTTTCATCTCGCTGCTCATGAGCTGGACGGCTGCTGCCATT 539
QY 141 ValHisAlaThrAsnSerGlnArgProArgLysLeuAlaGluLysAlaValTyrVal 160
DB 540 GTCACAGCCCAACACATCAAGAGCCAAAGAACTGCTGCTGAAGGACAGCTATAGTG 599
QY 161 G1ValTyrPheProAlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSer 180
DB 600 GGGCTCTGGATCCAGCCCTCTCTGCTGACTATACCTTACTTCTTGGCCGAGCTAGC 659
QY 181 GlnGlyAspIleSerGlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSer 200
DB 660 CAGGGGACATCATGACGGGGATGACAGTACATCTGTGACCGCTTTCACCCGATAGC 719
QY 201 LeuTyrMetValValPheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIle 220
DB 720 CTGTGGATGGTGTGTTCAATTCACAGATATAGTGGTCTCATCTGCGCGGATC 779

QY 221 ValIleLeuSerCysTyrCysIleIleIleSerLysLeuSerHisSerLysGlnHisGln 240
DB 780 GTGATCTCTCTGCTTACTAGCATCATCATCTCTAAGCTGTACACATCCAGGCGCACAG 839
QY 241 LysArgLysAlaLeuLysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrLeu 260
DB 840 AACCGCAAGGCCCTCAAGACAGACATCATCTCTGCTTCTTCTGCTGCTGCTG 899
QY 261 ProTyrTyrValGlyIleSerIleAspSerPheIleLeuGlyValIleLysGlnGly 280
DB 900 CCATATTATGTGGGATGACATGACATGCTCTTATCTTTTGGAGTCAATCAAGCAAGA 959
QY 281 CysAspPheGluSerIleValHisLysTyrIleSerIleThrGluAlaLeuAlaPhePhe 300
DB 960 TGTGACTTCAGAGCATTTGTGCAAGAGTGTGATTCATCATACAGAGCCCTGCTTCTTC 1019
QY 301 HisCysCysLeuAsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerAla 320
DB 1020 CACTGTGCTGCAACCCATCTCTATGCTTCTGCTGCGGCGCAAGTTCAAAAGCTCTGCC 1079
QY 321 GlnHisAlaLeuAsnSerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLys 340
DB 1080 CAGCATGCACTCAACTCCATGACAGAGAGGCTCCAGCTCAAGATCTTCCAAAGGAAG 1139
QY 341 ArgGlyGlyHisSerSerValSerThrGluSerGluSerSerPheHisSerSer 359
DB 1140 CGCGGTGGACATCTTCCGCTCTCCAGGAGTCAAGATCTCCAGTTTCTCACTGCAC 1196

RESULT 3
AAZ38553
ID AAZ38553 standard; cDNA; 1059 BP.
XX
AC AAZ38553;
DE 22-FEB-2000 (first entry)
XX
XX Human CXK-chemokine receptor-4 (CXCR-4) cDNA.
KW CXK-chemokine receptor-4; CXCR-4; stromal cell derived factor-1; SDF-1;
KW ligand; chemotaxis; inflammation; G-protein-coupled receptor;
KW signal transduction; CD4-independent; HIV-1; infection; proliferation;
KW transformation; tumorigenesis; cancer; tumour; overexpression; brain;
KW breast; colon; lung; melanoma; glioblastoma; inhibition; growth arrest;
KW diagnosis; prognosis; marker; proliferative disorders; antisense;
KW therapy; treatment; premalignant condition; hypertrophy; degenerative
KW disorder; Parkinson's disease; Alzheimer's disease; growth deficiency;
KW hypoproliferative disorder; physical trauma; lesion; ischaemia; wound;
ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1059
FT /*tag= a
FT /product= "Human CXCR-4"
XX
PN W09950461-A1.
XX
XX 07-OCT-1999.
PD
XX
PF 29-MAR-1999; 99WO-US07431.
XX
XX 30-MAR-1998; 98US-0079916.
PR 16-OCT-1998; 98US-0104656.
XX
XX (NMBI-) NORTHWEST BIOTHERAPEUTICS INC.
PA Murphy GP, Boynton AL, Sehgal A;
PI
XX
DR WPI: 2000-052634/04.
DR P-PSDB: AAY52507.
XX
PT Use of CXCR-4 and SDF-1 as markers for diagnosis and treatment of e.g.

PT tumors, degenerative disorders, growth deficiencies, hyper- and
PT hypoproliferative disorders, physical trauma, lesions and wounds
XX
PS Disclosure; Fig 14; 138pp: English.

CC This sequence represents cDNA encoding CXCR-4 chemokine receptor-4
CC (CXCR-4). Chemokine receptors play an important role in the chemotaxis of
CC T-cells and phagocytic cells to areas of inflammation. CXCR-4 is a member
CC of the G-protein-coupled receptor family, which is involved in signal
CC transduction, and its ligand is stromal cell derived factor-1 (SDF-1,
CC AAV52508). CXCR-4 also mediates CD4-independent infection by HIV-1.
CC CXCR-4 has now been found to have a role in the aberrant proliferative
CC behaviour of a number of cell types, including numerous primary tumours
CC and derived cell lines. CXCR-4 is involved in cell transformation and
CC tumorigenesis, particularly in brain, breast and colon tumours. It was
CC found to be overexpressed in several brain tumour derived cell lines and
CC primary brain tumour tissues, breast tumour tissues, colorectal
CC adenocarcinoma, lung carcinoma and melanoma cell lines. CXCR-4 expression
CC was required for the continuous proliferation of glioblastoma cancer
CC cells, and inhibition of its gene function resulted in growth arrest.
CC Conversely, overexpression resulted in enhanced and rapid cellular
CC proliferation. CXCR-4 and SDF-1 can be used as markers for the diagnosis
CC and prognosis of cell proliferative disorders, and antisense
CC oligonucleotides complementary to at least a portion of an RNA transcript
CC of a CXCR-4 gene can be used to inhibit hyperproliferation of a tumour
CC cell. Agents that inhibit CXCR-4 function can be used for treating or
CC preventing a disease or disorder involving cell overproliferation, e.g.,
CC brain cancer, breast cancer, colon cancer, prostate cancer and B cell
CC lymphoma, and also premalignant conditions, benign tumours,
CC hyperproliferative disorders, and benign dysproliferative disorders. They
CC can also be used for treating e.g., cirrhosis of the liver, Keldoid
CC formation, psoriasis, benign tumours, fibrocystic conditions and tissue
CC hypertrophy. Compounds that promote CXCR-4 function can also be used for
CC preventing or treating a disease or disorder involving a deficiency in
CC cell proliferation, or treating a condition where cell proliferation
CC would be desirable. Such diseases include degenerative disorders (e.g.,
CC Parkinson's disease, Alzheimer's disease), growth deficiencies,
CC hypoproliferative disorders, physical trauma, lesions (e.g., those caused
CC by ischaemia), and wounds.

XX Sequence 1059 BP; 244 A; 301 C; 232 G; 282 T; 0 other;

Alignment Scores:

Pred. No.: 1,84e-187 Length: 1059
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
21 Gaps: 1

US-09-367-052-2 (1-359) x AA238553 (1-1059)

OY 6 ValSer11eTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
DB 10 ATCAGATATATACCTTCTCAGTATACACCGAGGAATGGGCTCAGGGCATATGACTCC 69
OY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
DB 70 ATGACGAGAACCCGTTCCGTGAGAAATCTCAATTCATTAATCTTCGCCGCCACC 129
OY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
DB 130 ATCTACTCATCATCTTCTTAATGCTGATGCGCAATGGATGCTGCTCCGCGCAG 189
OY 66 GLTYTfGILySLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
DB 190 GGTTCACAGAAAGAACTGAGAACATGACGACGACAACTACAGGCTGACCTGACGTGCC 249
OY 86 AspIleLeuPheValIleThrLeuProPheTyrPalaValAspAlaMetAlaAspTyrPyr 105
DB 250 GACCTCCTCTTGTATACACGCTCCCTCTGCGGCGATTGATGCCGCAACGTGATC 309
OY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125

DB 310 TTGGGAACTTCTTATGCAAGGACATGATCATCTACAGTCAACCTTACAGCACT 369
OY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
DB 370 GTTCCTATCTCTGCTTCATCATGTCGACCCCTTACCTGCGCATCTCCACCCACCAAC 429
OY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
DB 430 AGTCAGAGGCCAAGAAAGCTGTGGCTGAAGAGTGCTATGTGGCTGTGGATCCCT 489
OY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnLysAspIleSer 185
DB 490 GCCCTCTCTGCTGATCTCCGACTCATCTTGGCAACGTC-----ACT 534
OY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerIleuTrpMetValVal 205
DB 535 GAGGCAATGACAGATATATCTGTGACCCCTTACCCCAATGACTGTGGGTGTGTG 594
OY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
DB 595 TTCCAGTTTCAGCACATCATGTTGGCTTATCTCTGCTGATGTCTATCTCTGCTGCTC 654
OY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
DB 655 TATTCATTATCATCTCAAGCTGTCACACTCCAAAGGCGCACAGAGCGCAAGGCCCTC 714
OY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
DB 715 AAGACCACAGTATCTCTCATCTGCTTCTTGGCTGTGGCTGCTTACTACATTTGGG 774
OY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleGlyGlnGlyCysAspPheGluSer 285
DB 775 ATCAGATGATGCTCTTATCTCTCTCGGAATCATCAACAGAGGTCGATTTGAGAAC 834
OY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
DB 835 ACTGTGCACAGAGGATTTCCATTCACAGGCGCTTACTTCTCCACTGTGTCTGAAC 894
OY 306 ProIleLeuTyrAlaPheLeuGlyValAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
DB 895 CCCATCTCTATGCTTTCTCTTGAGCCCAATTTAAACCTCTGCGCAGACCCACTCCACC 954
OY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyLysHisSer 345
DB 955 TCTGTAGACAGAGGGTCCAGCCTCAAGATCTCTCCAAAGGAAGAGAGCTGACATTTCA 1014
OY 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
DB 1015 TCTGTTCCACTGAGTGTGATGCTTCAAGTTTTCACCTCCAGC 1056

RESULT 4
AAH99952 standard; cDNA; 1059 BP.
XX
XX AAH99952;
AC 18-JUN-2002 (first entry)
XX
XX
DE CXCR4 encoding sequence.
XX
XX Human Chemokine receptor 4; CXCR4; gene; human; ss;
KW Human chromosome 2q21; HIV-1.
XX
XX Homo sapiens.
OS
XX
XX Key
XX Location/Qualifiers
FT variation
FT replace (414,T)
FT /tag= a
FT /standard_name= "single nucleotide polymorphism"
FT replace (783,T)
FT /tag= b
FT /standard_name= "single nucleotide polymorphism"

PA (KISH/) KISHIMOTO T.
 XX Kishimoto T, Nagasawa T, Tachibana K;
 PI WPI: 1999-591042/50.
 DR P-PSDB: AAY39933.
 XX
 XX Vascularisation inhibitors
 XX
 PS Disclosure: Page 48-49; 63pp; Japanese.
 XX
 CC This sequence encodes the human CXCR4 protein. The invention relates to
 CC remedies inhibiting neovascularisation, remedies for solid cancer,
 CC remedies for diseases pathologically caused by neovascularisation and
 CC tissue repairing agents containing as the active ingredient a substance
 CC capable of potentiating CXCR4. Based on a finding that vascularisation is
 CC inhibited in a CXCR4 knockout mouse, it becomes possible to prepare
 CC remedies inhibiting vascularisation which contain as the active
 CC ingredient a substance capable of potentiating CXCR4, remedies for solid
 CC cancer, remedies for diseases pathologically caused by neovascularisation
 CC and tissue repairing agents containing as the active ingredient a
 CC substance capable of potentiating CXCR4. It is also possible to establish
 CC methods for treatment with the use of these remedies.
 SQ Sequence 1588 BP; 396 A; 375 C; 334 G; 483 T; 0 other;

Alignment Scores:

Pred. No.: 3 36e-187 Length: 1588
 Score: 1678.50 Matches: 319
 Percent Similarity: 95.48% Conservative: 19
 Best Local Similarity: 90.11% Mismatches: 11
 Query Match: 89.90% Indels: 5
 DB: 20 Gaps: 1

US-09-367-052-2 (1-359) x AA227610 (1-1588)

QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
 DB 10 ATCACTATATACACTTACAGTACAGTACACCGAGAAATGGGCTCAGGGGACTATGACTCC 69
 QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
 DB 70 ATGAAGGAACCTGTTCCGTGAGAAATGCTAATTTCAATAAATCTCTCGCCACC 129
 QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
 DB 130 ATCTACTCCATCATCTTCTTACTGCGCATGTGGCAATGAGATTTGGTCACTCTGCTCATG 189
 QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
 DB 130 GGTTCACGAGAAACTGAGAGCATGACGACAGTACAGGCTGCACCTGTCACTGGCC 249
 QY 86 AspleuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTyrPyr 105
 DB 250 GACCTCTCTTGTATACAGGCTCTCTTGGGAGTTGATGCGGTGGCAAACTGATAC 309
 QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
 DB 310 TTTGGGAACCTTCTTGCAGAGCATGCTCATCTACACAGTCAACCTCTACAGCAGT 369
 QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
 DB 370 GTTCCTATTCCTGGCTTATGAGTGTGACGCTACCTGCGCATGCTGCACGCCACAC 429
 QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
 DB 430 AGTCAGAGGCCAAGAGAGCTGTGGCTGAAAAGGGGTCTATGTGGGCTGAGTCCCT 489
 QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
 DB 490 GCCCTCTGCTGACTATTCCTCCGACTTCACTTTTGGCAACGTC-----AGT 534
 QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205

DB 535 GAGGACAGATGACAGATATATCTGTGACCGCTCTACCCCAATGACTTGGGTGTTGCG 594
 QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
 DB 595 TTCCAGTTTCACACATCATGCTTGCCCTTATCTGCGGTATGTGATCATCTCTGCTGC 654
 QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlnHisGlnLysArgLysAlaLeu 245
 DB 655 TATTCATATATCTCTCCAGCTGTACACTCCAGGCGCCACAGACAGCGCAGGCCCTTC 714
 QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
 DB 715 AAGACACAGATCATCTCTCTGCTTCTTCCGCTGTGGCTGCTGCTTACTACTATTGGG 774
 QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheLeuSer 285
 DB 775 ATCAGCATTCGACTCTCTATCTCTCTGGAATCAACAGCAGGCTGTGAGTGTGAGAAC 834
 QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
 DB 835 ACTGTGCACAGATGATTTTCCATCACCGAGGCCCTTACTTTTCCACTGTTGTCTGAAAC 894
 QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
 DB 895 CCCATCTCTATGCTTCTCTGAGCCAAATTTAAACCTCTGCCACAGACACTCACAC 954
 QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyHisSer 345
 DB 955 TCTGTGAGAGGAGGCTCCAGCCTCAAGATCTCTCTCAAGGAAACGAGGTGACATTCA 1014
 QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
 DB 1015 TCTGTTCCACTGAGTCTGAGTCTTCAAGTTTTCCTCCAGC 1056

RESULT 6
 AAA61656
 ID AAA61656 standard; DNA; 1664 BP.
 XX
 AC AAA61656;
 XX
 DT 23-OCT-2000 (first entry)
 XX
 DE Human CXC chemokine receptor (CXCR4) cDNA.
 XX
 KW CXCR4: human CXC chemokine receptor 4; HIV infection inhibition;
 KW expression inhibition; antisense therapy; ss.
 XX
 OS Homo sapiens.
 OS
 PH Key Location/Qualifiers
 FT primer_bind 67..90
 FT /tag= a
 FT /bound_moiety= "Antisense oligonucleotide SEQ ID NO:1
 FT primer_bind 73..96
 FT /tag= b
 FT /bound_moiety= "Antisense oligonucleotide SEQ ID NO:2
 FT primer_bind 61..83
 FT /tag= b
 FT /bound_moiety= "Antisense oligonucleotide SEQ ID NO:3
 FT (AAA61653)"
 FT (AAA61654)"
 PN WO200031271-A1.
 PD 02-JUN-2000.
 XX
 PD 24-NOV-1999; 99WO-JP06534.
 XX
 PR 24-NOV-1998; 98JP-0332760.
 XX
 PA (HISM) HISAMITSU PHARM CO LTD.

XX Iijima O, Goto T, Shimada T;
 XX WPI: 2000-400081/34.
 XX
 XX Antisense oligonucleotide, useful as inhibitor in preventive or remedy
 PT for HIV infection with high therapeutic efficacy
 XX
 XX Example 1; Page 17-18; 21pp; Japanese.
 XX
 CC The invention relates to human CXCR4 chemokine receptor 4 (CXCR4)-specific
 CC antisense oligonucleotide (AA61652-A61654). The oligonucleotides
 CC hybridise with the CXCR4 gene and/or CXCR4 RNA, thereby preventing its
 CC expression. As CXCR4 plays a role in HIV infection, the antisense
 CC oligonucleotides act as inhibitors of this process. Compositions
 CC containing the antisense oligonucleotides are useful as prophylactic
 CC or therapeutic agents for HIV infection. Such compositions are highly
 CC efficacious for inhibiting infection with HIV. The present sequence
 CC represents a human CXCR4 cDNA.

Sequence 1664 BP: 414 A; 398 C; 359 G; 493 T; 0 other;

Alignment Scores:

Pred. No.: 3.6e-187 Length: 1664
 Score: 1678.50 Matches: 319
 Percent Similarity: 95.48% Conservative: 19
 Best Local Similarity: 90.11% Mismatches: 11
 Query Match: 89.90% Indels: 5
 DB: 21 Gaps: 1

US-09-367-052-2 (1-359) x AA61656 (1-1664)

QY 6 ValserIleYrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
 ID :::
 DB 86 ATCAGTATATACCTTACAGTAACTACACCGAGCAATGGCTCAGGGGACTATGACTCC 145
 QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
 ID :::
 DB 146 ATGAAGGAACCCGTTCCGTGAGAAATAATCTAATTCAATAAATCTCTCCGCCACC 205
 QY 46 IleYrPheIleIlePheLeuThrGlyTLeValGlnGlnGlyLeuValIleLeuValMet 65
 ID :::
 DB 206 ATCTACGTCATCATCTTCTTAACGTGCAATGCGCAATGATGATGATGATGATGATG 265
 QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
 ID :::
 DB 266 GGTACCAAGAAAGACAGAGCATGACGAGCAAGACAGTACGCTGACGTGCGCC 325
 QY 86 AspleuLeuPheValIleThrLeuProPheThrAlaValAlaMetAlaAspTrpTyr 105
 ID :::
 DB 326 GACCTCCTCTTTCATCAGCCGCTTCCCTTGGGCAAGTGTGCGGCAAACTGGTAC 385
 QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
 ID :::
 DB 386 TTGTGGAGACTTCATATGCAAGGAGTCATGTCATACAGCAACCTCTACAGCAGT 445
 QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
 ID :::
 DB 446 GTCCTCATCTCGGCTTCATGACTGTGACCGCTACCTGCGCATGCTCCACGCCAAC 505
 QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
 ID :::
 DB 506 AGTCAGAGGCCAAGAGAGCTGTGCTGAAAGAGGTGCTGTGGGCTGTGATCCCT 565
 QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
 ID :::
 DB 566 GCCCTCGCTGACTATTTCCGCACTTCACTTTGCCAAGC-----AGT 610
 QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
 ID :::
 DB 611 GAGGCAAGTGCACATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGTGTGTG 670
 QY 206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSerCys 225

DB 671 TTCAGTTTCAGCAGCATGATGCTGGCTTATCCTGCTGATGTATGTCATCTGCTGC 730
 QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlnLysArgLysAlaLeu 245
 DB 731 TATTCATTTATCATCTCAAGCTGTCACACTCCCAAGGCCACCAAGGCCCAAGCCCTC 790
 QY 246 LysThrThrValIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
 DB 791 AAGACACAGTCATCTCATCTGCTTCTTCCCTGCTTGGCTGCTTACTACATTGGG 850
 QY 266 IleSerIleAspSerPheIleLeuGluGlyValIleLysGlnGlyCysAspPheGluSer 285
 DB 851 ATCAGATCGACTCTTCATCTCTCTGGAATCATCAAGCAAGGGTGTGAGTTGAGAAC 910
 QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysLysLeuAsn 305
 DB 911 ACTGTGACACAGTGTGATTTCCATCACCAGGCCCTTACTCTTTCACACTGTGTGTGAC 970
 QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerAlaGlnHisAlaLeuAsn 325
 DB 971 CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAACCTGTGCCAGCAGCTCACC 1030
 QY 326 SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgGlyHisSer 345
 DB 1031 TCTGTGACAGAGGGGTCCAGCTCAAGATCCTCTCCAAAGAAAGCAGGTGACATTCA 1090
 QY 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
 DB 1091 TCTGTTCACACTGAGTGTGAGTCTTCAAGTTTTCATCTCCACG 1132
 DB
 RESULT 7
 AAZ40014
 ID AAZ40014 standard; DNA; 1664 BP.
 XX
 AC AAZ40014;
 AC
 AC
 DT 14-FEB-2000 (first entry)
 DT
 XX
 DE CXCR4 coding sequence.
 XX CXCR4; inhibitor; antisense oligonucleotide; anti-HIV agent;
 KW HIV infection; therapy; ss.
 KW
 XX
 OS Synthetic.
 EN JP11285391-A.
 XX
 PD 19-OCT-1999.
 PD
 XX 18-NOV-1998; 98JP-0327942.
 XX
 XX 19-NOV-1997; 97JP-0335085.
 XX
 PA (HISM) HISAMITSU PHARM CO LTD.
 PA (TOAG) TOA GOSSEI CHEM IND LTD.
 XX
 DR WPI: 2000-026817/03.
 XX
 PT An oligonucleotide used as an anti-HIV agent - inhibits CXCR4 protein
 PT expression
 PT
 PS Disclosure: Page 5-6; 6pp; Japanese.
 XX
 CC This sequence represents a CXCR4 coding sequence. The invention relates
 CC to antisense oligonucleotides that hybridise specifically with
 CC chromosomal DNA and/or RNA encoding a CXCR4 protein, and inhibit the
 CC expression of the CXCR4 protein. The antisense oligonucleotides can be
 CC used in an anti-HIV agent. The oligonucleotides and the anti-HIV agent
 CC are highly effective as a preventive and treating agent for HIV
 CC infection.
 XX
 Sequence 1664 BP: 414 A; 398 C; 359 G; 493 T; 0 other;

Alignment Scores:

Pred. No.:	3,66-187	Length:	1664
Score:	1678.50	Matches:	319
Percent Similarity:	95.48%	Conservative:	19
Best Local Similarity:	90.11%	Mismatches:	11
Query Match:	89.90%	Indels:	1
	21	Gaps:	5

US-09-367-052-2 (1-359) x AA240014 (1-1664)

```

QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 86 ATCAGTATATACACTGATGATACACACGAGAAATGGCTCAGGGAGATATAGATCC 145

QY 26 AsnIysGluProCysPheArgSPGLuAsnValHisPheAsnAqIlePheLeuProThr 45
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 146 ATGAGAGAACCTCTTCCGTAAGAAATGCTTAATTCATTAATAATCTCTCCACACC 205

QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 206 ATCTACATCCATCATCTCTTAAGTGGCATGTGGCAATGATGGATGCTCATG 265

QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 266 GGTACACAGAGAAACAGACGATGACGACAAAGTACAGGGCTGACCTGTAGTGCC 325

QY 86 AspleuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTyrTyr 105
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 326 GACCTCCTCTTGTGATCAGCCCTTCTCGGCACTGATGCGCGCAACTGGTAC 385

QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 386 TTGTGGAACTCTCTATCAAGGCGAGTCCATCTCATCAACAGCAACTCTACAGCAGT 445

QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 446 GTCTCATCTCGGCTTATAGTGTGACCGCTACCTGCGCATGTCACAGCCACGAC 505

QY 146 SerGlnArgProArgLysLeuAlaGluLysAlaValTyrValGlyValTyrP16Pro 165
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 506 AGTACAGGCCAAGAGAGCTTTGGCTGMAAAGTGGCTCATGTGGCGTGTGATCCCT 565

QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 566 GCCCTCTGCTGACTATATCCGACTTCATCTTCCAAAGCNC-----AGT 610

QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrPmetValVal 205
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 611 GAGCGACATGACAGATATATCTGTGACCGCTTACCCCAATGACTTGTGGTGTG 670

QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 671 TTCCAGTTTACGACATCATGTTGGCTTATCTGCTGATATTCATCTCTCTCTGC 730

QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 731 TATTCGATTTATCATCTCAAGCTTCACACCTCAAGGCGCCACGAGACCGACGCCCTC 790

QY 246 LysThrThrValIleLeuIleLeuAlaPhePheIleCysTyrPleuProTyrTyrValGly 265
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 791 AAGGCCACAGTACCTCATCTGCTTCTTCCGCTGTGGCTGCTTACTATCATATGGG 850

QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 851 ATCAGCATCAGCTCTTCATCTCTCTGAAATCATCAAGCAGAGGTTGAGTTGACAAC 910

QY 286 IleValHisLysTyrPleuSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 911 ACTGTGCACAGTGTGATTTCCATCACCAGAGCCCTACTCTTCTCCACTGTGCTCAAC 970

QY 306 ProIleuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

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Db 971 CCATCTCTATGCTTCTTGGAGCCCAATTTAAACCTCTGCGCCAGCAGACTACACC 1030

QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyHisSer 345
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1031 TCTGTGACAGAGGGTCCACCTCATACATCTCTCCAAAGAAAGCAGGTGACATTC 1090

QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1091 TCTGTTCACACTGACTGCTGCTTCAAGTTTTCATCTCAGC 1132

RESULT 8
ABK83803 standard; cDNA; 1670 bp.
ID ABK83803
XX
AC ABK83803;
XX
DT 14-Aug-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #374.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; peridominal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
PN W0200228999-A2.
XX
PD 11-Apr-2002.
XX
PE 03-Oct-2001; 2001MO-US10821.
XX
PR 03-Oct-2000; 2000US-237189P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Beezer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR WPI: 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity
XX
PS Claim 1; SEQ ID No 374; 114bp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation,
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA, M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating

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expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publihed_pct-sequences.

Sequence 1670 BP; 418 A; 400 C; 361 G; 491 T; 0 other:

Alignment Scores:

Pred. No.:	3.62e-187	Length:	1670
Score:	1678.50	Matches:	319
Percent Similarity:	95.48%	Conservative:	19
Best Local Similarity:	90.11%	Mismatches:	11
Query Match:	89.90%	Indels:	5
DB:	24	Gaps:	1

US-09-367-052-2 (1-359) x ABN95645 (1-1670)

```
6 ValSerIleYrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
82 ATCAGTATATACACTTCAGTACTACACCGAAGAAATGGCTCGGGGACTATGACTCC 141
26 AsnIlysgIuproCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProthr 45
142 ATGAAGGAACCCGTGTTCCGTGAAGAAATGCTATATTCAATAAATCTTCCTGCCACCC 201
46 IleYrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
202 ATCTACCTCAATCCTCTTACCTGCGATTTGGGCAATGATGGTCACTCTGCTCATG 261
66 GlyTyrGlnIlySlyLeuArgSerMetThrAspIlySlyTyrArgLeuHisLeuSerValAla 85
262 GCTTACCGAAGAAACTGAGAAGCTGACGCAAGTACAGGCTCCACCTGCTCAGTGGCC 321
86 AspleuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTyrTyr 105
322 GACCTCCTCTTGTGATCATCAGCTTCCCTTGTGGGAGTTGATGCGCTGGAACCTGGTAC 381
106 PheGlyIlySlyPheLeuCysIlyAlaValHisIleIleYrThrValAsnLeuTyrSerSer 125
382 TTTGGGAACCTTCATATGACAGGCACTGCATCATCAACAGTCAACCTCTACAGCAGT 441
126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
442 GTCCCTCATCTGGCTTATCATGCTGAGACCGCTACCTGGCCATGCTCCAGCCGCCAC 501
146 SerGlnArgProArgIlySlyLeuAlaGluIlyAlaValTyrValGlyValTyrIlePro 165
502 AGTCAGAGCCCAAGAACTGTGGCTGAAGAGTGCTCATGTGGCTGGATCCCT 561
166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnIlyAspIleSer 185
562 GCCCTCCCGACATATCCGACATTCCTTTCGCAACGTC-----AGT 606
186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrMetValAla 205
607 GAGGCAAGTACAGATATATCTGTGACCGCTTTCACCCCAATGACTTGTGGGTGTGG 666
206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSerCys 225
667 TTCCAGTTTCAGCACATCATGTGGCTTATTCGCTGGATGATGTCATCTGTCCTGCG 726
226 TyrCysIleIleIleSerIlySlyLeuSerHisSerIlySlyGlnIlySlyArgIlyAlaLeu 245
727 TATTGCATATATCATCTCCACAGCTGCACATCCCAAGGCCACCGAAGGCCCTCC 786
246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysThrPleuProTyrTyrValIly 265
787 AAGACACAGCATCTCTATCTGCTTCTGCTGCTGCTGCTGCTGCTTACTACATTTGG 846
266 IleSerIleAspSerPheIleLeuLeuGlyValIleIlySlyGlnIlyCysAspPheGluSer 285
```

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DB 847 ATCAGATCAGCATCTTCCTCATCTCCGTAATCATCAAGCAAGGCTGTGACTTGAGAAC 906
QY 286 IleValHisIlySlyTyrPheIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
DB 907 ACTGGCACAAGTGGATTTCCATCATCCAGGCCCCCTAGCTTTCTTCCACTGTGTGCTGAC 966
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaIlySlyPheIlySlySerSerAlaGlnHisAlaLeuAsn 325
DB 967 CCCATCTCTATGCTTCTTCTTCGAGCCCAATTTTAAACCTCTGCCACAGCAGCTACCC 1026
QY 326 SerMetSerArgGlySerSerLeuIlySlyLeuSerIlySlyIlySlyArgGlyIlyHisSer 345
DB 1027 TCTGTGACGACAGAGGCTCCAGCCCTCAAGATCTCTCCAAAGGAAAGCGAGTGGACATTTCA 1086
QY 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
DB 1087 TCTGTTCACCTGAGTGTGAGTCTTTCAGATTTTCATCTCCAGC 1128

RESULT 10
AA165467
ID AA165467 standard; DNA; 1679 BP.
XX
AC AA165467;
XX
DT 10-DEC-2001 (first entry)
XX
DE Nucleotide sequence of a human polynucleotide.
XX
KW Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV;
KM gp120; C-type lectin; ICAM3; HIV entry; T cell; macrophage;
KN HIV infection; ss.
XX
OS Homo sapiens.
XX
PN WO200164752-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06322.
XX
PR 02-MAR-2000; 2000US-0517605.
XX
PA (UYNV) UNIV NEW YORK STATE.
XX
PA (UYNV-) UNIV NIJMEGEN.
XX
PI Litman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;
XX
DR WPI; 2001-602565/68.
XX
PT An antibody for the treatment or prevention of HIV-infection comprises
PT a gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding
PT of DC-SIGN due to concomitant conformational change -
XX
PS Disclosure; Page 126-127; 131pp; English.
XX
CC The specification describes an antibody which is specific for an
CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN
CC or is exposed upon gp120 binding of DC-SIGN due to concomitant
CC conformational change. DC-SIGN is a receptor that is specifically
CC expressed on dendritic cells and facilitates infection of T lymphocytes
CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin.
CC DC-SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
CC with high affinity. The antibody of the invention inhibits the trans
CC enhancement of HIV entry into a T cell or macrophage facilitated by
CC dendritic cells. The antibody is useful to treat or prevent HIV
CC infection. The present sequence represents a human polynucleotide,
CC which is used in the course of the invention.
XX
SQ Sequence 1679 BP; 407 A; 400 C; 368 G; 504 T; 0 other:

Alignment Scores:
Pred. No.: 3.65e-187 Length: 1679
Score: 1678.50 Matches: 319
```

Percent Similarity: 95.488
 Best Local Similarity: 90.118
 Query Match: 89.908
 DB: 22
 Gaps: 1

US-09-367-052-2 (1-359) x AA165467 (1-1679)

```

QY 6 ValSerIleTyrThrSerAspAntySerGluGluValGlySerGlyAspTyrAspSer 25
DB 98 ATCAGATATATACACTTACATATACACTACCGAGAAATGGCGCAGGACATATGACTCC 157
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
DB 158 ATGAAGAGAACCTGTTCCGTGAGAAATGCTAATTCATAATTCATCTCCGCCACAC 217
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
DB 218 ATCTACTCCATCATCTTCTTAATGCGCATTTGGCGCAATGGATGGTCATCTCGTCATG 277
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgPheHisLeuSerValAla 85
DB 278 GGTACACAGAAAGAACTGAGAACATGACGAGACGACGACGCTGACCTGTCAGTGGCC 337
QY 86 AspLeuLeuPheValIleThrLeuProPheTyrPalValAspAlaMetAspTyrTyr 105
DB 338 GACCTCTCTTGTTCATCAGCGCTTCCCTCTGGCGAGTGGATGCGCGCAACCTGCTAC 397
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
DB 398 TTGGGAACTCTCTTAAGCAAGCGACATGTCATATACACATCAACCTCTACACAGT 457
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
DB 458 GTCCATATCTCTGCTTCACTCATCTGACCGCTTACCTGCGCTCCAGCGCACACAC 517
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTyrIlePro 165
DB 518 AGTCAGAGGCGCAAGAGAGCTGTGGCTGAAGAGTGTCTATGTGGCGTGCATGCCCT 577
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
DB 578 GCCCTCTCTGACATATCCCGCATCTTATCTTGGCCACAGCTC-----AGT 622
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrPheValVal 205
DB 623 GAGCGCATATGACGATATATCTGTGACCGCTTACCCCAATACTCTTG6GGTGTG 662
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
DB 683 TTCACGTTTCAGACATCATGTTGGCTTATCTGCTGCTGATTTGTCATCTGCTGCTG 742
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
DB 743 TATGTGATTATATCTCCAGGCTGTCCACTCCAGGCGCCACGAGCGCCGCTC 802
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysThrLeuProTyrTyrValGly 265
DB 803 AAGACACAGTCACTCTCATCTG6GCTTCTTCTGCTGCTGCTGCTTACTTCACTTGG 862
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnLysCysAspPheGlnSer 285
DB 863 ATCAGCATGAGCCTTCATCTCCCGAATATCATCAGCAAGGAGTGTGAGTTGAGAAC 922
QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
DB 923 ACTGTCCACAGAGGTATTCATCCACGAGGCCCTGCTTCTTCCACTGTTGCTGAGAC 982
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerIleGlnHisAlaLeuAsn 325
DB 983 CCATCTCTATGCTTCTTCTGAGCCAAATTTAAACCTCTGCCCCAGCGACGACTGACC 1042
QY 326 SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgGlyHisSer 345
DB 1103 TCTGTTCCACTGAGTGTGAGTCTTCAAGTTTCACTCCAGC 1144

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DB 1043 TCTGTGAGCAGAGGCTCCAGCCTCAAGATCTCTCCAAAGAGGAGGTGACATTTCA 1102
QY 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
DB 1103 TCTGTTCCACTGAGTGTGAGTCTTCAAGTTTCACTCCAGC 1144

RESULT 11
AADI2801
ID AADI2801 standard; DNA: 1679 BP.
XX
AC AADI2801;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human neuropeptide Y (NPY) Y3 receptor DNA.
XX
KW Human; neuropeptide Y; NPY; bone disease; bone mass; gene therapy;
KW cerebrospinal fluid; CSF; inositol phosphate; IP; Paget's disease;
KW fracture; extracellular signal-regulated kinase; ERK; osteoporosis;
KW osteopenia; bone metastasis; neurotransmitter; osteogenic;
KW NPY Y3 receptor; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 89..1147
FT /tag= a
FT /product= "Human neuropeptide Y (NPY) Y3 receptor"
XX
PE WO200153477-A1.
XX
PD 26-JUL-2001.
XX
PE 22-JAN-2001; 2001MO-US02040.
XX
PR 20-JAN-2000; 2000US-0489872.
XX
PA (BAYLOR ) BAYLOR COLLEGE MEDICINE.
XX
AM (AMLI/) AMLING M.
XX
PI Amling M, Karsenty G, Ducey P;
XX
DR WPI; 2001-488709/53.
XX
DR P-PSDB; AAED06930.
XX
PT Treating or preventing reduced bone mass, e.g. osteoporosis, by
PT reducing the level of neuropeptide Y activity in blood or cerebrospinal
PT fluid.
XX
PS Example 7; Page 84-85; 102pp; English.
XX
CC The present invention relates to a method for treatment or prevention of
CC bone diseases characterized by loss of bone mass, comprises administering
CC to a mammal a compound that lowers the level of neuropeptide Y (NPY) in
CC the serum or cerebrospinal fluid (CSF) or a compound that lowers the
CC level of inositol phosphate (IP) or extracellular signal-regulated kinase
CC (ERK). The method is specifically used to treat (including by gene
CC therapy) or prevent osteoporosis, osteopenia or Paget's disease, but may
CC also be used e.g., in cases of fractures or bone metastases. These
CC diseases may also be diagnosed by detecting elevated NPY levels,
CC including monitoring of treatment, assessing efficacy of compounds in
CC clinical trials and for identifying subjects at risk. The present
CC sequence is a human NPY Y3 receptor DNA.
XX
SO Sequence 1679 BP; 407 A; 400 C; 368 G; 504 T; 0 other;

Alignment Scores:
Pred. No.: 3,65e-187
Score: 1678.50
Percent Similarity: 95.488
Best Local Similarity: 90.118
Query Match: 89.908
Matches: 319
Conservative: 19
Mismatch: 11
Indels: 5
Gaps: 1

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US-09-367-052-2 (1-359) x AAD12801 (1-1679)

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OY 6 ValSerIleThrPheSerAspAsnTyrSerGluGluValAlGlySerGlyAspTyrAspSer 25
DB 98 ATCAGTATATACACTTACATACACGAGAAATGGCTCAGGGGACTATGACTCC 157
OY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
DB 158 ATGAGAGAACCCGTTTCCGTGAAGAAATGCTATTTCAATAAATCTTCCTGCCACC 217
OY 46 IleTyrPheIleIlePheLeuThrGlyIleValAlGlyAsnGlyLeuValIleLeuValMet 65
DB 218 ATCACTCCATCACTCTTAACTGAGCATTTGGGCAATGATGATGATCATCTGTCATG 277
OY 66 G1TyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLysLeuValAla 85
DB 278 GGTACCAAGAAAGAACTGAGAGACATGACGACAGATGACGCTGACCTGTGCTGCC 337
OY 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
DB 338 GACCTCTCTTTGTCATCAGCGCTCCCTCTGGGCAATGATGGCGGCAACTGGTAC 397
OY 106 PheGlyLysPheLeuGlyLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
DB 398 TTTGGGAACCTCTATGCAAGGACATGATCATACAGTCAACCTCTACAGCAGT 457
OY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrIleuAlaIleValHisAlaThrAsn 145
DB 458 GTCTCTCTCTGGCTTCATCATGCTGGACCGCTACTGCGCATCGTCCAGCCACAC 517
OY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValAlaTrpPhePro 165
DB 518 AGTCAGAGGCCAAGAAAGCTGTTGGTGAAAGGTGATGATGTTGGCGTGGATCCCT 577
OY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
DB 578 GCCCTCTCTGCTATATCCGACCTCATCTTGGCCACAGCTC-----AGT 622
OY 186 GlnGlyAspAspArgTyrIleGlyAspAspArgLeuTyrProAspSerLeuTrpMetVal 205
DB 623 GAGCGACATGACGATATATCTGTGACCGCTTCTACCCCAATGACTGTGGTGGTGTG 682
OY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
DB 683 TTCAGATTTCAGACATCATGATGTTGGCTTATCCTGCTGATGTCATCTGCTGTC 742
OY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
DB 743 TATTGCAATTCATCTCCAGCTGTCACTCCAGAGGCCACAGAGGCCAGGCCCTC 802
OY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
DB 803 AAGACCAACATCATCCATCCTGCTGGCTTCTTGGCCCTGTTGGCTTCTCATATTGG 862
OY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
DB 863 ATCAGATCATGACTCTTCATCTCTGGAATATCATCAAGAGGTGAGTTTGAGAAC 922
OY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
DB 923 ACTGTGACAAAGGATTCATCCATCCAGAGCCCTTCTTCCACTGTTGCTGAC 982
OY 306 ProIleLeuTyrAlaPheLeuGlyAlaValPheLysSerSerIleGlnHisAlaLeuAsn 325
DB 983 CCCATCTCTATGCTTTCTTGAGAGCAAAATTTAAACCTCTGCGCCACGCACTCACC 1042
OY 326 SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
DB 1043 TCTGTGAGCAGAGGTCCAGCCTCAAGATCTCTCCAAAGAAAGGAGGTGACATTTCA 1102
OY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359

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DB 1103 TCTGTTTCACAGTCTGAGTCTTCAAGTTTCACTCCAGC 1144
RESULT 12
AA080521
ID AA080521 standard; cDNA; 1737 BP.
XX
AC AA080521;
XX
DE 18-JUL-1995 (first entry)
XX
XX Human monocyte PF4AR cDNA.
XX
KW Interleukin-8 receptor; IL-8 receptor; PF4AR;
KW platelet factor superfamily receptor; monocyte; chemotactic;
KW inflammation; inflammatory disease; arthritis; emphysema; cystic;
KW fibrosis; colitis; bronchitis; meningitis; therapeutic; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 91..1149
FT /tag= a
XX
XX W09428931-A.
XX
XX 22-DEC-1994.
XX
XX 07-JUN-1994; 94WO-US06380.
XX
XX 11-JUN-1993; 93US-0076093.
XX
XX (GETH ) GENENTECH INC.
XX
XX Chuntharapal A, Hebert C, Kim KJ, Lee J;
XX
XX WPI, 1995-036114/05.
XX
XX DR P-PSDB; AAR68812.
XX
XX PT Treatment of inflammatory disorders - by administering an
XX antibody capable of binding a platelet factor 4 superfamily
XX receptor polypeptide
XX
XX PS Disclosure; Page 54-56; 83pp; English.
XX
XX 2 PF4AR members were identified by probing lambda libraries from
XX human monocyte-like cell line HL-60 and human peripheral blood
XX lymphocytes using a large fragment of IL-8 receptor DNA (full
XX sequence given in AA080520). The nucleotide sequences of the 2
XX PF4ARs are given in AA080521 and AA080522, and their respective
XX amino acid sequences in AAR68812 and AAR68813.
XX
SQ Sequence 1737 BP; 454 A; 411 C; 373 G; 499 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 3.84e-187 Length: 1737
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 16 Gaps: 1
US-09-367-052-2 (1-359) x AA080521 (1-1737)
OY 6 ValSerIleThrPheSerAspAsnTyrSerGluGluValAlGlySerGlyAspTyrAspSer 25
DB 100 ATCAGTATATACACTTACATACACGAGAAATGGCTCAGGGGACTATGACTCC 159
OY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
DB 160 ATGAGAGAACCCGTTTCCGTGAAGAAATGCTATTTCAATAAATCTTCCTGCCACC 219
OY 46 IleTyrPheIleIlePheLeuThrGlyIleValAlGlyAsnGlyLeuValIleLeuValMet 65

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Db	220	ATCAGCCATCAGCATCTTTAAAGCGGAGCTGTGGGCAATGGATTGGCATCTCGTCATGG	279
Qy	66	GLYTYRGLINLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla	85
Db	280	GGTTACCAAGAAACCTGAGAGAGCATGACGGACAAGTACAGAGCTGCACCTCTCATGTGGCC	339
Qy	86	AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetCalaAspTrpIyr	105
Db	340	GACCTCCTCTTTGTCATCAGCCTTCCTCCCTTCCTGGGAGGTGATGCCGTGGCAAACTGGTAC	399
Qy	106	PheGLysPheLeuCysLysAlaValHisIleLeuTyrThrValAsnLeuTyrSerSer	125
Db	400	TTTGGGAACCTCCATGCAAGGAGCTCATGTCTCATCTACAGAGTACACTCTACAGCAGT	459
Qy	126	ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn	145
Db	460	GTCTTCATCTCCGGCCTTCATCAGTCTGGACCGCTACCTGGCCATGCTGCACGCCACAAAC	519
Qy	146	SerGlnArgProAlaGlyLysLeuLeuAlaLysAlaValIlyTyrValGlyValThrPro	165
Db	520	AGTAGAGAGCCACAGAAAGCTGTGGCTGAAAAAGGTGTCATAGTGGCGCTGAGTCCCT	579
Qy	166	AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer	185
Db	580	GCCCTCCCTCGTCATCTATTCGCCGACTTCATCTTTGCCAACGTC-----AGT	624
Qy	186	GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal	205
Db	625	GAGGAGATGACAGATATATCTGTGACCGCTTCATCCCAATGACTTGTGGGTGTGTG	684
Qy	206	PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys	225
Db	685	TTTCAGATTTCAGCAGCATCATGCTGGCCCTTATCCGCTGTGATGTGTCATCTGCTGC	744
Qy	226	TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu	245
Db	745	TATTCGATATTCATCTCCAAAGCTGTACACATCTCCAAAGGGCCACAGAAAGCCAAAGCCCTC	804
Qy	246	LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly	265
Db	805	AAGACACAGATCATCTCATCTGCTTCTTCGCCCTGTGGCTCCTTACTACATTTGGG	864
Qy	266	IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheLeuSer	285
Db	865	ATCAGACATCGACTCCTTCATCTCCTCTGGAAATCATCAAGCAAGAGGTGTGAGTTGAGAAC	924
Qy	286	IleValHisLysTrpIleSerIleThrGlnAlaLeuAlaPhePheHisCysCysLeuAsn	305
Db	925	ACTGTGCAAGAGTGGATTTCATCTACCCAGAGGCCCTTCTTCTTCTCAGTGTCTGAAAC	984
Qy	306	ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn	325
Db	985	CCCATCTCTATGTCTTCTCTGGAGCCAAATTTAAACCTCTGCCACAGACCACTCACCC	1044
Qy	326	SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyLysIleSer	345
Db	1045	TCTGTGACCAAGAGGTCTCAGGCTCAAGATTCCTTCCAAAGGAACGAGGTGGACATCTCA	1104
Qy	346	SerValSerThrGlnSerGlySerSerSerPheHisSerSer	359
Db	1105	TCTGTTCCTACAGTGAAGTGTGAGTCTTCAAGTTTCTTCACTCAGC	1146
RESULT 13			
AAQ99007			
ID	AAQ99007	standard; cDNA; 1737 BP.	
XX	AAQ99007:		
XX			
XX	26-MAR-1996	(first entry)	
XX			
DE		Chemokine superfamily receptor coding sequence.	
XX			
KW		Interleukin; IL-8; inflammation; psoriasis; dermatitis;	

XX	rhematoid arthritis; inflammatory bowel disease;
KW	chronic lung inflammation; treatment; antibody;
KW	affinity purification; detection; ss.
XX	
OS	Homo sapiens.
XX	
PN	US5440021-A.
XX	
PD	08-AUG-1995.
XX	
PF	29-MAR-1991; 91US-0677211.
XX	
PR	25-FEB-1994; 94US-0202056.
PR	29-MAR-1991; 91US-0677211.
XX	
PA	(CHUN/) CHUNTHARAPAI A.
PA	(HEBE/) HEBERT C.
PA	(KIMK/) KIM K. J.
PA	(LEEJ/) LEE J.
XX	
PI	Chuntharapai A, Hebert C, Kim KJ, Lee J;
DR	WPI: 1995-283151/37.
DR	P-PSDB: AAR80757.
XX	
PT	New antibodies against interleukin 8 type B receptor - used to treat
PT	or prevent inflammation, also for detecting receptor expression and
PT	purificn.
XX	
PS	Example 2; Columns 47-50; 62pp; English.
XX	
CC	Antibodies directed against the interleukin-8 receptor B can be used
CC	to treat or prevent inflammation e.g. psoriasis, dermatitis,
CC	rheumatoid arthritis and particularly inflammatory bowel disease and
CC	chronic lung inflammation. When immobilised, these antibodies may
CC	be used to detect interleukin-8 receptor B expression in cells and
CC	tissues and for affinity purification of interleukin-8 receptor B
CC	from cells. This sequence is an additional chemokine superfamily
CC	receptor which was identified by probing lambda libraries of genomic
CC	cDNA from a human monocyte-like cell line (L-60) and human peripheral
CC	blood lymphocytes using a large fragment of the interleukin-8 type
CC	A receptor DNA (See AMQ99006).
XX	
SO	Sequence 1737 BP; 454 A; 411 C; 373 G; 499 T; 0 other;
XX	
Alignment Scores:	
Pred. No.:	3,84e-187 Length: 1737
Score:	1678.50 Matches: 319
Percent Similarity:	95.48% Conservative: 19
Best Local Similarity:	90.11% Mismatches: 11
Query Match:	89.90% Indels: 5
DB:	16 Gaps: 1
XX	
US-09-367-052-2 (1-359) x AAQ99007 (1-1737)	
QY	6 ValSerIleTyrrThrSerAspAsnTyrSerGluGluValIglYSerGlyAspTyrAspSer 25
DB	::: ::: ::: ::: ::: ::: ::: ::: :::
100 ATCAGTATATACACTTCACGTAACACTACCGACGAGAAATGGCGTCGAGGAGACTATGACTCC 159	
QY	26 AsnIleGluPrCysSphearGAspGluAsnValAlhSphAsnAlGlllePheLeuProThr 45
DB	::: ::: ::: ::: ::: ::: ::: :::
160 ATGAGAGAACCCGTTTCGCTGAGAAATGCTAAATTTCAATAAATCTTCCTCCACCC 219	
QY	46 IleTyrPheIleIlePheLeuThrGlyIleValIglYAsnGlyLeuValIleLeuValMet 65
DB	::: ::: ::: ::: ::: ::: ::: :::
220 ATCTACCTCCATCTCTCTTTAACTGCGCATTTGGCGCAATGATTTGGTCATCTCTGATG 279	
QY	66 GlyTyrGlnLysLysLeuArGySerMetThrAspLysTyrArgLeuHISLeuSerValAla 85
DB	::: ::: ::: ::: ::: ::: ::: :::
280 GGTACACAGAGAAACTGAGAGCATGACGACAGCAAGTACAGGCTGCACCTGCAGTGCGCC 339	
QY	86 AspLeuLeuPheValIleThrIleuProPheTrrPalalaValAspAlaMetAlaAspTrrTyr 105
	::: ::: ::: ::: ::: ::: ::: :::

```
D 340 GACCTCCTTTTTCATCAGCGCTTCCTTCCTGGGAGTTGATCCGTGGCAAACTGATC 399
Q 106 PheGlyLysPheLeuLysLysAlaValHisIleIleTyrThrValAsnLeuTyrSer 125
D 400 TTTGGGAAGCTTCTATGCAAGGAGGAGTCCATGATCTACACGTCACCTTACAGAGT 459
Q 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaTyrAsn 145
D 460 GTCTCATCTCGCTTCATCAGCTGGACCGCTACCTGGCCATCGTCCAGCCACCAAC 519
Q 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTyrPhePro 165
D 520 AGTCAAGGCGCAAGGAGGAGTGTGGCTGAAAGGTGCTATGTTGGCTGTGATCCCT 579
Q 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
D 580 GCCCTCTGCTGATCTCCGACTTCATCTTTGCCAACGTC-----AGT 624
Q 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrMetValVal 205
D 625 GAGCAGAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTGTGGTGTGG 684
Q 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
D 685 TTCCTAGTTTCAGCAGATCATGATGTTGGCTTATCTGCTGGTATTTGTCATCTGCTG 744
Q 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
D 745 TATTCATTTATCATCTCCAAAGCTGTCACACTCCAAAGGCGCACAGAGCGCCCTC 804
Q 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrLeuProTyrTyrValGly 265
D 805 AAGACCAAGTCAATCTCATCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864
Q 266 IleSerIleLeuSerPheIleLeuLeuGlyValIleGlnGlnLysAspPheGlnSer 285
D 865 ATCAGCATGACTCTTCATCTCTGCTGGAATCATCAAGCAAGGAGTGTGAGAAC 924
Q 286 IleValHisLysTyrPheSerIleThrGlnAlaLeuAlaPhePheHisCysLeuAsn 305
D 925 ACTGTCACAGATGATTCATCCATCCAGGCGCTTCTTCCACAGTGTGTGTGAGAC 984
Q 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
D 985 CCCATCTCTATGCTTCTCTGGAGCCAAATTTAAACCTCTGCCAGCAGCAGCTCACC 1044
Q 326 SerValSerThrGlnSerSerLeuLysIleLeuSerGlyLysArgGlyGlyHisSer 345
D 1045 TCTGTACGAGAGGAGGAGGAGCTCAAGATCTCTCCAAAGGAAAGGAGGAGTGTGACATTC 1104
Q 346 SerValSerThrGlnSerSerLeuLysIleLeuSerGlyLysArgGlyGlyHisSer 359
D 1105 TCTGTTCCAGTGTGAGTGTGATTTTCACTTCCAGC 1146
```

RESULT 14

ABI97982
ABI97982 standard: cDNA; 1059 BP.

ABI97982:

18-FEB-2002 (first entry)

Non-endogenous human GPCR cDNA, SEQ ID NO: 484.

Human: G protein-coupled receptor; GPCR; non-endogenous; mutant;

constitutively activated GPCR; agonist; disease; ss.

Homo sapiens.

Synthetic.

MO200177172-A2.

18-OCT-2001.

```
XX 05-APR-2001; 2001WO-US11098.
PF 07-APR-2000; 2000US-195747P.
PR (AREN-) ARENA PHARM INC.
PI Lehmann-Brunnsma K, Liaw CW, Lin I;
XX MPI: 2001-648759/74.
DR P-PSDB; ABB56346.
XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT disease treatment, comprises contacting candidate compounds with
PS versions of GPCRs -
XX Example 2; Page 284-285; 394pp; English.
XX The invention relates to G protein-coupled receptors (GPCRs) for which
CC the endogenous ligand has been identified. Non-endogenous
CC constitutively activated versions of known GPCRs are used in the
CC invention for the direct identification of candidate compounds as
CC receptor agonists, inverse agonists or partial agonists. Such
CC agonists are useful as therapeutic agents for diseases or disorders
CC associated with GPCRs. The present sequence encodes a non-endogenous
CC version of a known human GPCR.
SQ Sequence 1059 BP; 246 A; 299 C; 233 G; 281 T; 0 other;
```

Alignment Scores:

Pred. No.:	9,366-187	Length:	1059
Score:	1672.50	Matches:	318
Percent Similarity:	95.20%	Conservative:	19
Best Local Similarity:	89.83%	Mismatches:	12
Query Match:	89,588	Indels:	5
DB:	23	Gaps:	1

US-09-367-052-2 (1-359) x ABI97982 (1-1059)

```
Q 6 ValSerIleTyrThrSerAspAsnTyrSerGlnGluValGlySerGlyAspTyrAspSer 25
D 10 ATCAGATATATACATTCATCAGATATACATCCAGGAAATGGCTCCAGGAGCTATATCTCC 69
Q 26 AsnLysGluProCysPheArgAspGlnAsnValHisPheAspArgIlePheLeuProThr 45
D 70 ATGAAGGAACCTGTTTCCGTGAGAAATGCTAATTTCAATAAATCTCTCTGCCACAC 129
Q 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
D 130 ATCTACTCCATCATCTTCTTAACTGAGCATTTGGGCAATGATGATGCTGCTGCTGCTG 189
Q 66 GlyTyrGlnLysLysLeuAsnSerMetThrAspLysTyrArgLeuHisSerValAla 85
D 190 GGTACCCGAAAGAAATCTGAGAGCATGACGAGCAAGTACAGGCTCCACCTGCACTAGGCC 249
Q 86 AspLeuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTyrTyr 105
D 250 GACCTCCTCTTGTGATACGCTTCTCTGAGAGTTGATGCGGTGGCAAACTGTGATC 309
Q 106 PheGlyLysPheLeuLysLysAlaValHisIleIleTyrThrValAsnLeuTyrSer 125
D 310 TTTGGGAAGCTTCTATGCAAGGAGGAGTCCATGATCTACACAGTCAACCTTACAGCAGT 369
Q 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaTyrAsn 145
D 370 GTCTCATCTCGCTTCATCAGCTGGACCGCTACCTGGCCATCGTCCAGCCACCAAC 429
Q 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTyrPhePro 165
D 430 ACTCAGAGGCCAAGAGAGCTGTGGCTGAAAGGTGCTATGTTGGGCTGTGATCTCCT 489
Q 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
```


QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
 |||
 DB 810 TATTCATTATCATCTCCAGCTGCACACTCCAGGCCACCCAGCCAGCCCTC 869
 QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
 |||
 DB 870 AAGACCACAGTCATCTCATCTGCTTCTGCGCTGTGCTGCTTACTACTACTGCG 929
 QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGlnSer 285
 |||
 DB 930 ATCAGCATCGACTCTTCTATCTCTCTGGAATCATCAAGCAAGGCTGTGAGTTGAGAAC 989
 QY 286 IleValHisLysTrpIleSerIleThrGlnAlaLeuAlaPhePheHisCysCysLeuAsn 305
 |||
 DB 990 ACTGTGCACAGAGTGATTTCCATCCACGAGGCCCTAGCTTCTCTCTCCACTGTGTCTGAAC 1049
 QY 306 ProIleLeuTyrAlaPheLeuGlyValAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
 |||
 DB 1050 CCCATCTCTATGCTTCTTCTGAGCCAAATTTAAACCTCTGCCACGACGACTCAC 1109
 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
 |||
 DB 1110 TCTGTGACGACAGGGGTCCAGCTCAAGATCCTCTCCAAAGGAAGCGAGGTGGACATTCA 1169
 QY 346 SerValSerThrGlnSerGlnSerSerSerPheHisSerSer 359
 |||
 DB 1170 TCTGTTCCACGAGCTGAGCTTCAAGTTTTCACCTCCAGC 1211

Search completed: July 12, 2003, 17:14:34
 Job time : 222 secs

Db ATCAGTATATACACTTGCATGATACACGAGGAAATGGCTCAGGAGCATATGATCC 145
QY AsnlysgluprocyspheargspgluasValHisphesnaargllepheleuprothr 45
Db ATGAGGAGAACCTGTTCCGGAAGAAATTAATTCATATAAATCTCCGCCACC 205
QY IlethyphelilelephetheuthrGlylleValglsnnglyleuValilleleValmet 65
Db ATCTACCTCATCTTCTTAAGTCAGATGTTGGCAATGGATGGCATCTGCTCATG 265
QY 66 GlytyrGlnlyslsleuAargSerMetThrAspLysTyrArgleuHisleuSerValala 85
Db GGTACACAGAGAAACAGAGAGATGACGACACAGAGCCGCACTGCTGAGTGGCC 325
QY AspleuLeupheValillethleupropheThrpalalaValasplametalasptPtyr 105
Db GACCTCTCTTGTTCATCAGCCTTCCCTTCTGGGCACTGATGCGCGGCAAACTGGTAC 385
QY PheGlyLysPheleucysLysAlaValHislleIleTyrThrValAsnLeuTyrSerSer 125
Db TTGGAAGACTCTCATGCAAGGAGTCATGTCATACACAGTCAACCTCTACAGCAGT 445
QY 126 ValleuIleleuAlaIlephelleSerleuAspArgTyrIleuAlaIleValHisAlaThrAsn 145
Db GTCTCTCATCTGCGCTTCATCAGTCTGACCGCTACCTGCGCATCTGACGCGCACAC 505
QY 146 SerGlnArgProArgLysleuLeuAlaGlyAlaValTyrValGlyValIleTyrIlePro 165
Db AGTAGAGAGCCAGAGAAAGCTGTTGGCTGAAAGGTGTCATGTGGCGCTGATCCCT 565
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnIleAspIleSer 185
Db GCCCTCTCTGATCTATCCGACTTCATCTTCCCAAGCTC-----AGT 610
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrMetValVal 205
Db GAGGCAATGACAGATATATCTGTGACCGCTTACCCCAATGATGATGGTGGTGTG 670
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleleuSerCys 225
Db TTCCAGTTTCAGCATCATCATGTTGGCTTATCTGCTGATGTTCATCTCTCTCTGC 730
QY 226 TyrCysIleIleIleSerLysleuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db TATGCAATATCATCTCCAAAGCTGTCTCACTCCAAAGGCGCACAGAGCCCAAGGCTC 790
QY 246 LysThrThrValIleleuIleleuAlaIlePhePheAlaCysTyrLeuProTyrTyrValGly 265
Db AAGACACAGATCTCTCATCTGCTGCTTCTGCGCTGTGGCTGCTTACTCATGATGGG 850
QY 266 IleSerIleAspSerPheIleleuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db ATGAGCATGCACTCTCATCTCTCTGGAATATATCAAGCAAGGCTGTGATTTGANAAC 910
QY 286 IleValHisLysTyrIleSerIleThrGlnAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db ACTGTGACAAAGTGATTCATCATCACCAGAGCCCTTACTTCTCCACTGTGCTGAAC 970
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaValPheLysSerSerIleGlnHisAlaIleAsn 325
Db CCATCTCTTATGCTTCTTCTGAGCCAAATTTAAACCTCTGCGCAGCAGCATTCACC 1030
QY 326 SerMetSerArgLysSerleuLysIleLeuSerLysGlyLysArgGlyLysHisSer 345
Db TCTGTGAGCAGAGGCTCAGCCTCAAGATCTCTCTCCAAAGAAAGCAGAGTGGACATTC 1090
QY 346 SerValSerThrGlnSerGlnSerSerSerPheHisSerSer 359
Db TCTGTTCACAGTGTGATGCTTCAAGTTTCACTCCAGC 1132
Db 1091 TCTGTTCACAGTGTGATGCTTCAAGTTTCACTCCAGC 1132

RESULT 2
US-09-517-605-14
; Sequence 14, Application US/09517605

; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Liltman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeek, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517, 605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-517-605-14

Alignment Scores:

Pred. No.:	3,13e-188	Length:	1679
Score:	1678.50	Matches:	319
Percent Similarity:	95.48%	Conservative:	19
Best Local Similarity:	90.11%	Mismatches:	11
Query Match:	89.90%	Indels:	5
DB:	4	Gaps:	1

US-09-367-052-2 (1-359) x US-09-517-605-14 (1-1679)

QY 6 ValSerIleTyrThrSerAspAsnTyrSerGlnGluValGlySerGlyAspTyrAspSer 25
Db ATCAGTATATACACTTGCATGATACACGAGGAAATGGCTCAGGAGCATATGATCC 157
QY 26 AsnlysgluprocyspheargspgluasValHisphesnaargllepheleuprothr 45
Db ATGAGGAGAACCTGTTCCGGAAGAAATTAATTCATATAAATCTCCGCCACC 217
QY 46 IlethyphelilelephetheuthrGlylleValglsnnglyleuValilleleValmet 65
Db ATCTACCTCATCTTCTTAAGTCAGATGTTGGCAATGGATGGCATCTGCTCATG 277
QY 66 GlytyrGlnlyslsleuAargSerMetThrAspLysTyrArgleuHisleuSerValala 85
Db GGTACACAGAGAAACAGAGAGATGACGACACAGAGCCGCACTGCTGAGTGGCC 337
QY 278 SerGlnArgProArgLysleuLeuAlaGlyAlaValTyrValGlyValIleTyrIlePro 165
Db AAGACACAGATCTCTCATCTGCTGCTTCTGCGCTGTGGCTGCTTACTCATGATGGG 397
QY 106 PheGlyLysPheleucysLysAlaValHislleIleTyrThrValAsnLeuTyrSerSer 125
Db TTGGAAGACTCTCATGCAAGGAGTCATGTCATACACAGTCAACCTCTACAGCAGT 457
QY 126 ValleuIleleuAlaIlephelleSerleuAspArgTyrIleuAlaIleValHisAlaThrAsn 145
Db GTCTCTCATCTGCGCTTCATCAGTCTGACCGCTACCTGCGCATCTGACGCGCACAC 517
QY 146 SerGlnArgProArgLysleuLeuAlaGlyAlaValTyrValGlyValIleTyrIlePro 165
Db CCATCTCTTATGCTTCTTCTGAGCCAAATTTAAACCTCTGCGCAGCAGCATTCACC 577
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnIleAspIleSer 185
Db GCCCTCTCTGATCTATCCGACTTCATCTTCCCAAGCTC-----AGT 622
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrMetValVal 205
Db GAGGCAATGACAGATATATCTGTGACCGCTTACCCCAATGATGTTGGGCTGTG 682
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleleuSerCys 225
Db TTCCAGTTTCAGCATCATCATGTTGGCTTATCTGCTGATGTTCATCTCTCTCTGC 742

QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
|||||
Db 743 TATTCATATATCATCTCCAAAGCTGTACACTCCAAAGGGCCACAGAGGCCAGGCCCTC 802
QY 246 LysThrThValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
|||||
Db 803 AAGACACAGCATCATCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 862
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
|||||
Db 863 ATCAGCATGATCTCTTCTCATCTCTCTGGAATCATCATCAAGGAGGTGATGTTGAGAAC 922
QY 286 IleValHisLysTrpLysSerIleThrGlnAlaLeuAlaPhePheHisCysCysLeuAsn 305
|||||
Db 923 ACTGTGACAAAGTGGATTTCCATCCAGCCGACGCTGCTTCTTCCACTGTTGTGTGAGAC 982
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
|||||
Db 983 CCCATCTCTATGCTTCTCTGAGGCAAAATTTAAACCTGCTGCCAGACGACACTCACCC 1042
QY 326 SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgLysGlyHisSer 345
|||||
Db 1043 TCTGTGACAGAGGCTCCAGCCTCAAGATCTCTCCAAAGAGAAAGGAGGTGAGACATTGA 1102
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
|||||
Db 1103 TCTGTTCCACTGATGCTGATCTTCAATTTTCACTCCAGC 1144

RESULT 3
US-08-202-056-4
Sequence 4, Application US/08202056

Patent No. 5440021

GENERAL INFORMATION:

APPLICANT: Chuntharapai, Anan

APPLICANT: Hebert, Caroline

APPLICANT: Kim, Kyung Jin

APPLICANT: Lee, James

TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Path (Genentech)

CURRENT APPLICATION DATA:

FILING DATE: US/08/202,056

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/677211

FILING DATE: 29-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: 706P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/952-5530

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1737 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-202-056-4

Alignment Scores:
Pred. No.: 3,296-188
Score: 1678.50
Percent Similarity: 95.488
Best Local Similarity: 90.118
Query Match: 89.908
DB: 1
Gaps: 1
US-09-367-052-2 (1-359) x US-08-202-056-4 (1-1737)

QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
:::|||||
Db 100 ATCAGTATATACACTTCACTCACTAAGTACACGAGAAATAGGCTCAGAGGAGTATGACTCC 159
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgLlePheLeuProThr 45
|||||
Db 160 ATGAAGAACCCCTGTTCCGTGAGAGAAATGCTAAATTTCAATTAATTTCTTCTGCCACCC 219
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
|||||
Db 220 ATCTACTCCATCATCTTCTTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 279
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
|||||
Db 280 GGTACACAGAGAACTGAGAGCATGACGAGCAAGTACAGGCTGACCTGTCAGTGGCC 339
QY 86 AspLeuLeuPheValIleThrLeuProPheThrPalaValAlaMetAlaAspTrpTyr 105
|||||
Db 340 GACCTCTCTTCTTCTCATCAGCTTCTCTCTCTGAGGAGTGTAGTCCGTGCAAACTGTAC 399
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
|||||
Db 400 TTGGGAACCTTCTTATGACAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT 459
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
|||||
Db 460 GTCCTCATCTGCGCTTATCATGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGT 519
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
|||||
Db 520 ACTCAGAGGCCAAGAGCTGTGGCTGAAAGGTGTATGTGGCTGTGAGTCCCT 579
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnLysAspIleSer 185
|||||
Db 580 GCCCTCTCTGCTATCTCCAGCTTCTTCCAGCTC-----AGT 624
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
:::|||||
Db 625 GAGGACAGTACAGATATATCTGTGACGCTTCTTACCCCAAGTGTGGGTGTGG 684
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyTyrIleValIleLeuSerCys 225
|||||
Db 685 TTCAGCTTCCAGCACATCATGTGTGGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 744
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
|||||
Db 745 TATTCATATATCATCTCCAAAGCTGTACACTCCAAAGGGCCACAGAGGCCAGGCCCTC 804
QY 246 LysThrThValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
|||||
Db 805 AAGACACAGCATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
|||||
Db 865 ATCAGCATGATCTCTTCTCATCTCTGGAATCATCATCAAGGAGGTGATGTTGAGAAC 924
QY 286 IleValHisLysTrpLysSerIleThrGlnAlaLeuAlaPhePheHisCysCysLeuAsn 305
|||||
Db 925 ACTGTGACAAAGTGGATTTCCATCCAGCCGACGCTGCTTCTTCCACTGTTGTGTGAGAC 984
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
|||||

Db 985 CCCATCTCTATAGCTTCTTGGAGCCAAATTTAAACCTTCCACAGCAGCTCACC 1044
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyLysSer 345
Db 1045 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGAAAGCGAGGTGACATTCA 1104
QY 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
Db 1105 TCTGTTTCCAGCTGAGTCTGAGTCTTCAAGTTTTCACCTCAGC 1146

RESULT 4

US-08-076-093A-3
Sequence 3, Application US/08076093A
Patent No. 5543503

GENERAL INFORMATION:

APPLICANT: Chuncharapal, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PFAA Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/076,093A

FILING DATE: 11-Jun-1993

CLASSIFICATION: 530

PRIOR APPLICATION NUMBER: 07/810782

FILING DATE: 19-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/677211

FILING DATE: 29-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: 706P2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530

TELEFAX: 415/952-9881

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1737 nucleotides

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

US-08-076-093A-3

Alignment Scores:

Pred. No.: 3,29e-188 Length: 1737
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 1 Gaps: 1

US-09-367-052-2 (1-359) x US-08-076-093A-3 (1-1737)

QY 6 ValSerIleThrThrSerAspAspTyrSerGluGluValGlySerGlyAspTyrAspSer 25
Db 100 ATCACTATATACACTTTCAGATTAACACCGAGGAATGGGCTCAGGGGACTATGACTCC 159

QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 160 ATGAAGAGAACCTGTTTCCGAGGAAATGCTATATTCATTAATCTCTCCACCACC 219
QY 46 IleThrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 220 ATCACTCCATCAATCTTCTTAACCTGGCATTTGGGCAATGATTTGATCTCTGTCATG 279
QY 66 GlyThrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 280 GGTTCACAGAAAGAACTGAGAGCATGACGAGCAAGATTCAGAGCTGACCTGTCACTGAGCC 339
QY 86 AspleuLeuPheValIleThrLeuProPheThrPalaValAspAlaMetAlaAspTyrTyr 105
Db 340 GACCTCCCTTTTGTTCATCAGCCTTCCCTTGGGAGATGATGGCGTGGCAACTGGTAC 399
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleThrValAsnLeuTyrSerSer 125
Db 400 TTTGGAACTTCCATGCAAGGAGGAGTCCATCTCATCTACAGATCAACCTTCACAGAGT 459
QY 126 ValIleuIleuAlaPheIleSerLeuAspArgTyrIleuAlaIleValHisAlaThrAsn 145
Db 460 GTCTCATCTGCGCTTCTATCATGCTGAGCCGCTACCGCTGCGCATCTCCACGCCACAC 519
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValIleGlyValTyrPhePro 165
Db 520 AGTCAGAGGCCAAGAAAGCTGTGGCTGAAGAAGGTCTATGTGGGTGTGATCCCT 579
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 580 GCCCTCCGCTGACTATATCCCGACTTCATCTTCCCAAGTCTC-----AGT 624
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrPheValIle 205
Db 625 GAGGACAGTGCAGATATATCTGTGACCGCTTCTTACCCCAATGACTGTGGTGTGTG 684
QY 206 PheGlnPheGlnHisIleMetValGlyLeuLeuProGlyIleValIleLeuSerCys 225
Db 685 TTCCAGTTTCAGCAGATCATGTGGCTTATCCGTGCTGATTTGATCATCTGCTGCTGC 744
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 745 TATTGCATTATCATCTCCAAAGCTGTCCACATCCAAAGGCCACAGAACGCCAGCCCTC 804
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrLeuProTyrTyrValGly 265
Db 805 AAGACACAGATCATCTATCTGCTTCTTCCGCTTGTGGCTGCTTACTACATTGGG 864
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db 865 ATCAGCATCGACCTCTCATCTCTCTGGAATTCATCAAGAGGGTGTGACTTTGAGAAC 924
QY 286 IleValHisLysTyrPheIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 925 ACTGTGCACAAAGTGAATTCATCAACGAGGCCCTTACCTTCTTCACATGTTGCTGAC 984
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 985 CCCATCTCTATAGCTTCTTCCGAGCCAAATTTAAACCTTCCGACAGCAGCTCACC 1044
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyLysSer 345
Db 1045 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGAAAGCGAGGTGACATTCA 1104
QY 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
Db 1105 TCTGTTTCCAGCTGAGTCTGAGTCTTCAAGTTTTCACCTCAGC 1146

RESULT 5

US-08-701-265-3
Sequence 3, Application US/0801265
Patent No. 5776457
GENERAL INFORMATION:

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: WinPalin (Genentech)
CURRENT APPLICATION NUMBER: US/08/284,586
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 nucleotides
TYPE: Nucleic Acid
STRANDNESS: Single
TOPOLOGY: Linear
US-08-284-586-3

APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
8-805-478-3

Alignment Scores:
Pred. No.: 3,296-188 Length: 1737
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 11
Best Local Similarity: 90.11% Mismatches: 19
Query Match: 89.90% Indels: 5
DB: 2 Gaps: 1

US-09-367-052-2 (1-359) x US-08-805-478-3 (1-1737)

QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
Db 100 ATCAGTATATACCTTTCAGTATACACCGAGAAATGGCTCAGGGAGTATGACTCC 159
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 160 ATGAGGAAACCTCTTCCGTGAGAAATGCTAATTCAATAAATCTTCTGCCACC 219
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 220 ATCTACTCCATCATCTTCTTACTGCAATTTGTGGCAATGGATTGCTCATCTCTGTCATG 279
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 280 GGTACCAAGAAACAGTGAAGCATGACGACAAAGTACAGGCTGCACCTCTGAGTGGCC 339
QY 86 AspLeuLeuPheValIleThrLeuProPheTyrPalaValAlaAspAlaAspTyrTyr 105
Db 340 GACCTCCTTTGTATCACCCTTCCCTTGGGACAGTTGACCGCTGCAAACTGGTAC 399
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 400 TTGTGGAACTTCATGCAAGGAGCTCATGTCTACACAGTCAACCTCTACAGCAGT 459
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 460 GTCTCATTCCTGGCTTCATAGTCTGACCGCTACCTGGCCATCGTCCACGCCACAC 519
QY 146 SerGlnArgProArgLysLeuLeuAlaGlyLysAlaValTyrValGlyValTyrIlePro 165
Db 520 AGTCAGAGGCCCAAGAGAGCTGCTGCAAAAGCTGCTATGTTGGGCTGCATCCCT 579
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 580 GCCCTCCTGGCTATTCCTCCGACTTATCTTATCTTCCCAACGCTC-----AGT 624
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrMetValVal 205
Db 625 GAGGACAGATGACAGATATATCTGACCGCTTACCCCATGACTTGTGGTGTGTG 684
QY 206 PheGlnPheGlnHisIleMetValGlyLeuLeuProGlyIleValIleLeuSerCys 225

Db 685 TTCAGTTTCAGACATCATGTTGGCTTATCTCCTGGTATGTATCATCTGTCTGC 744
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlnLysAsnGlyAlaLeu 245
Db 745 TATTGCAATATCATCTCCAAAGCTGCACACTCCAAAGGCCACGAGAGGCCCTC 804
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrPheProTyrTyrValGly 265
Db 805 AAGACCAAGCATCATCTCATCTGCTTCTTCCGCTGTGGCTTACTTACTATGGG 864
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db 865 ATCAGATCCGACTCTTCATCTCCTCGAAATCATCAAGCAGGCTGTGACTTGAGAAC 924
QY 286 IleValHisLysTyrPheIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 925 ACTGTGACAGATGATTCATCATCAGAGGCCCTAGCTTCTTCCACTGTGTGTGAC 984
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 985 CCCATCCTCATGCTTCTTCTGAGGCCAAATTTAAACCTCTGCCACAGCAGCTCACC 1044
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyLysHisSer 345
Db 1045 TCTGTGACAGAGAGGTCACAGCTCAAGATCCTCTCAAAAGAAAGCAGGTGACATTCA 1104
QY 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
Db 1105 TCTGTTCCACTGAGTCTGAGTCTTCAAGTTTCACTCCACG 1146

RESULT 8
US-08-802-627A-3
Sequence 3, Application US/08802627A
Patent No. 5892017
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Wood, William I.
TITLE OF INVENTION: NUCLEIC ACID ENCODING PFAA RECEPTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,627A
FILING DATE: 19-Feb-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2P1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1737 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 US-08-802-627A-3

Alignment Scores:

Score:	3.29e-188	Length:	1737
Percent Similarity:	1678.50	Matches:	319
Best Local Similarity:	95.48%	Conservative:	19
Query Match:	89.90%	Mismatches:	11
		Indels:	5
		Gaps:	1

US-09-367-052-2 (1-359) x US-08-802-627A-3 (1-1737)

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QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValAlaGlySerGlyAspTyrAspSer 25
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
100 ATCAGTATATACATCTTCAGATTAACACAGGAAATGGCGTCCAGGACATGATGATCC 159
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 26 AsnLysLubProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
160 ATGAAGAGACCCGCTTTCGTTGAGAAATGCTAATTTCATATAAACTTCTGCCCCACC 219
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
220 ATCTACCCATCATCTTCTTAACGCGATGTGGCGAATGGATTGGCATCTGCTGATG 279
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
280 GGTACACAGAAAGAACTGAGAGCATGACGACACAGACAGGCTGACCTGCTGAGTGCC 339
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 86 AspLeuLeuPheValIleThrLeuProPheThrAlaValAspIleMetAlaAspTyr 105
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
340 GACCTCCTTTGTCATCAGCAGCTTCCCTGCGGACGTTAGTGGCGAAACTGGTAC 399
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
400 TTTCGGAACTTCCTCATGCAAGGCGAGTGCATGTCATACACAGTCACCTCTACAGCAGT 459
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
460 GTCTCATCTCCGCTTCATCAGTCTGACCGGCTGACCTGCGCATCTGCGCACGCCAC 519
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 146 SerGlnArgProArgLysLeuLeuAlaGlyLysAlaValTyrValGlyValTyrIlePro 165
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
520 AGTCAGAGGCCAAGAGAGCTGTGGCTGAAAGGTGGTGTGCTGATGCTGATCCCT 579
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnLysAspIleSer 185
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
580 GCCCTCCTGGGACTATTCGCGAATTCATCTTCCCAACGTC-----AGT 624
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrPheValVal 205
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
625 GAGCAGATATACATATATCTGTGACCGCTTCCCAATGATGATGGCTGGCTGTG 684
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
685 TTCCAGTTTCAAGCAGATCATGTTGGCTTATCTGCTGCTGATTTGATCTCTCTCTCC 744
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlnHisGlnLysArgLysAlaLeu 245
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
745 TATTGATTTATCATCTCCAAAGCTGTCAACTCCCAAGGCGCCAGGAAGCGGAGCCCTC 804
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrPheProTyrTyrValGly 265
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
805 AAGACACAGATCATCTCATCTGCTTCTTCCCTGTTGGCGCTTACTACATTGGG 864
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnLysCysAspPheGlnSer 285
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
865 ATCAGCATCGATCTCTTCCTCTGTAATCATCATCAAGCAAGGCTGTGATTTGAGAAC 924
  
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QY 286 IleValHisLysTyrIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
925 ACTGTGACAGAAAGGATTTTCATTCACCGAGGCCCFAGCTTCTTCCACATGTTGTGAAAC 984
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
985 CCCATCCTCATCTCTTCTTCTTGGAGCCAAATTTAAACCTCTCCAGCAGCAGCTCACCC 1044
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyLysHisSer 345
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1045 TCTGTGAGCAGAGAGGCTCACCTCAAGATCTCTCCAAAGAAAGAGAGTGCATTTCA 1104
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1105 TCTGTTCCACGTGAGTCTGATCTTCAAGTTTCACTCCAGC 1146
  
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RESULT 9

US-08-801-238-3
 : Sequence 3, Application US/08801238
 : Patent No. 5919896

GENERAL INFORMATION:

APPLICANT: Lee, James
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: PF4A RECEPTOR
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESS: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/801,238
 FILING DATE: 19-Feb-1997
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/284586
 FILING DATE: 10-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/076093
 FILING DATE: 11-JUN-1993
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/810782

FILING DATE: 19-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P0706P2P1D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1737 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

US-08-801-238-3

Alignment Scores:

Pred. No.:	3.29e-188	Length:	1737
Score:	1678.50	Matches:	319
Percent Similarity:	95.48%	Conservative:	19
Best Local Similarity:	90.11%	Mismatches:	11
Query Match:	89.90%	Indels:	5
		Gaps:	1

US-09-367-052-2 (1-359) x US-08-801-238-3 (1-1737)

QY 6 ValSerIleThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
Db 100 ATAGATATATACCTTACATCTACACCGAGGAATAAGGCTGACGATGATGCTCC 159
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 160 ATAGAAGAACCCGTTTCCGTGAGAAATGCTAATTTCAATAAATCTTCCGCCACC 219
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 220 ATCTACTCCATCATCTTCTTAATGTCATGTCGCAATGATGATGTCATCTGTCATG 279
QY 66 GlyTyrGluLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 280 GGTACACAGAAAGAACTGAGAACATGACGACAGACAGCTGACCTGTCAGTGGCC 339
QY 86 AspleuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
Db 340 GACCTCTCTCTTTTCAACAGCTTCCCTTGTGGCAGTTGATCCCGGCAAACTGTGAC 399
QY 106 PheGlyLysPheLeuGlyLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 400 TTGGGAACTTCTTATGCAAGGCAAGTCATGTCATGACAGTCAACCTCTACAGCAGT 459
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 460 GTCTCTATCTGTGCTTCACTACATGTCGACCGCTGACCTGCGCCATGTCACCGCACAC 519
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
Db 520 AGTCAGAGGCAAGAAAGCTGTGGCTGAAGAGTGCTGATTTGGCGCTGTGATCCCT 579
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 580 GCCCTCTCTGCTGATCTCCGCACTTCATCTTGGCCAACTGCTC-----AGT 624
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetVal 205
Db 625 GAGCGCATGACGATATATCTGTGACCGCTTACCCCATCTGTTGGGTGGTGTG 664
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 685 TTCCAGTTTCAGACATCATCATGCTTGGCTTATCTGCTGCTGTGCTGCTGCTGCTG 744
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 745 TATTCATATATCATCTCAAGCTGTCACTCCAAAGGCGCAGAACGCGCAGGCCCTC 804
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
Db 805 AAGACACAGATCATCTCTGCTGCTGCTTCTTGGCTGTGGCTTACTCATTCATTGGG 864
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnLysCysAspPheGluSer 285
Db 865 ATCAGCATGACCTCTTCATCTCCCGAATATCATCAGCAAGGCTGTGATTTGAGAAC 924
QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 925 ACTGTCCACAAAGTGATTTCCATCACCAGAGGCCCTTCTTCCACTGTGTGTCGAA 984
QY 306 ProIleLeuTyrTrlAlaPheLeuGlyAlaLysPheLysSerSerIleGlnHisAlaLeuAsn 325
Db 985 CCCATCTCTATGCTTCTCTTGAGCCAAATTTAAATTTCCAGCAGCGAGCTACCC 1044
QY 326 SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgGlyHisSer 345
Db 1045 TCTGTAGAGGAGGCTGACGCTCAAGATCTCTCCAAAGAAAGCAGAGGTGCATTTCA 1104
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359

Db 1105 TCTGTTTCCAGTGTGATGCTGACGCTTTCACGTTTTCACCTCCAGC 1146

RESULT 10

US-08-801-228-3

Sequence 3, Application US/08801228

Patent No. 5922541

GENERAL INFORMATION:

APPLICANT: Lee, James

TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/801,228

FILING DATE: 19-Feb-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/284586

FILING DATE: 10-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/076093

FILING DATE: 11-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/810782

FILING DATE: 19-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P0706P2P1D3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1737 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

US-08-801-228-3

Alignment Scores:

Pred. No.: 3.29e-188

Score: 1678.50

Percent Similarity: 95.48%

Best Local Similarity: 90.11%

Query Match: 89.90%

DB: 2

Gaps: 1

US-09-367-052-2 (1-359) x US-08-801-228-3 (1-1737)

QY 6 ValSerIleThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
Db 100 ATAGATATATACCTTACATCTACACCGAGGAATAAGGCTGACGATGATGCTCC 159
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 160 ATAGAAGAACCCGTTTCCGTGAGAAATGCTAATTTCAATAAATCTTCCGCCACC 219
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65

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Db      220 ATCTACTCCATCATCTTCTTAACCTGGCATGTGGCAATGATGGTGCATCTGTGCATG 279
QY      66 GLTYTGTGTLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLy 85
        280 GGTTCACAGAAAGTACGAGACATGACGACAGACAGGCTGACCTGCTAGTGGCC 339
QY      86 ASPLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLy 105
        340 GACCTCTCTTTTTCATCAGCCTTCTTCTGCGCATGTCATCCGTGGCAACCTGTAC 339
Db      106 PheGLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLy 125
        400 TTTGGCAACTCTTATGCAAGGACGATGTCATCTACACAGTCAACCTGACACAGT 459
QY      126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
        460 GTCTCATCTGCTGCTTTCATCAGTGTGACGCTGACCTGCTGCTGCTGCTGCTGCTG 519
QY      146 SerGIArgProArgLysLeuLeuAlaGLySLySLySLySLySLySLySLySLySLySLy 165
        520 AGTCAGAGGCGCAAGAGAGCTGTGGCTGAAGAGTGTCTATCTTGGCGTGTGATCCCT 579
Db      166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
        580 GCCCTCTGCTGACTATTCCTCCGACTTCATCTTGGCAACGTC-----AGT 624
QY      186 GlnGLyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrPheValAla 205
        625 GAGGCAAGATGACAGATATATCTGTGACGCTTCTACCCCAATCACTGTGGGTGTGTG 684
Db      206 PheGlnPheGlnHisIleMetValGLyLeuIleLeuProGlyIleValIleLeuSerCys 225
        685 TTCAGATTCAGACATCATGATGTTGGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTG 744
QY      226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
        745 TATTGATTATATCTCCCAAGCTGTACACTCCCAAGGCGCACCAAGGCGCACGCTC 804
Db      246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysThrLeuProTyrTyrValGly 265
        805 AAGACCAACATCATCTCATCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 864
QY      266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGlnSer 285
        865 ATCAGCATGACATCTTCATCTCTCGAATATCATCAAGCAAGGAGTGTGAGAAC 924
Db      286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
        925 ACTGTGCACAAAGTGAATTCATCCATCACCAGGCGCTTCTTCTTCCACTGTGTCTGAAC 984
QY      306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerLagIlnHisAlaLeuAsn 325
        985 CCCATCTCTATGCTTCTTCTTGGAGCCAAATTTAAACCTCTGCGCACGACACTCACCC 1044
Db      326 SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgLysGlyHisSer 345
        1045 TCTGTGACAGAGAGGTCGACGCTCAAGATCCTCTCCAAAGGAAGGAGGTGACATTTCA 1104
QY      346 SerValSerThrGlnSerGlnSerSerSerPheHisSerSer 359
        1105 TCTGTTTCACATGAGTCTGAGTCTTCAAAGTTTCACTCCAGC 1146

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RESULT 11

US-09-104-296-3

Sequence 3, Application US/09104296

Patent No. 608/475

GENERAL INFORMATION:

APPLICANT: Lee, James

APPLICANT: Wood, William I.

TITLE OF INVENTION: PF4A Receptors

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

```

STREET: 1 DNA Way
City: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,296
FILING DATE: 24-June-1998
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/701265
FILING DATE: 22-AUG-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/664228
FILING DATE: 06-JUN-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-104-296-3
Alignment Scores:
Pred. No.: 3,296-188 Length: 1737
Score: 1678.50 Matches: 319
Percent Similarity: 95.488 Conservative: 19
Best Local Similarity: 90.118 Mismatches: 11
Query Match: 89.904 Indels: 5
DB: Gaps: 1
US-09-367-052-2 (1-359) x US-09-104-296-3 (1-1737)
QY      6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
        100 ATCAGATATATACACTTCAGATTAACACACCGAGAAATGCGCTCAGGGACATATGACTCC 159
Db      26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
        160 ATGAGGAAACCCGTGTTCCGTGAGAAATGCTTAATTTCAATAAATCTTCTGCGCCAC 219
QY      46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
        220 ATCTACTCCATCATCTTCTTAACCTGCGATGTGGGCAATGAGATTGGTCACTCTGCTCATG 279
Db      66 GLTYTGTGTLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLy 85
        280 GGTTCACAGAAAGTACGAGACATGACGACAGACAGGCTGACCTGCTAGTGGCC 339
QY      86 ASPLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLy 105
        340 GACCTCTCTTTTTCATCAGCCTTCTTCTGCGCATGTCATCCGTGGCAACCTGTAC 339
Db      106 PheGLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLySLy 125

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Db	400	TTTGGAACTTCATTCGAAGCAGTCCATTCATTCACAGTCAACCTTACAGCAGT	459
Qy	126	ValleuileuAlaPheileSerLeuAspArgTyrLeuAlaileValAlaIleThrAsn	145
Db	460	GTCTCATTCCTGGCTTCATTCAGTCTGGACCGTACCTGGCCACATGCTCCAGCCACCAAC	519
Qy	146	SerIlnArgProAlaGlySerLeuAlaAGIulysAlaValTyrValGlyValITrPlePro	165
Db	520	AGTAGAGAGCCCAAGGAAGCTTTGGCTGAAGAGGTGTATGTGGTGGCTGTGGATCCCT	579
Qy	166	AlaIleuLeuLeuTrIleProAspPheIlePheIleAspValSerGlnGlyAspIleSer	185
Db	580	GGCCTTCCTGCGATATATTCGCCGACTTCATCTTTGGCAACGTC-----AGT	624
Qy	186	GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal	205
Db	625	GAGCAGATGACAGATATATCTGTGACCGCTTACCCCAATGACTTGTGGGTGGTGTG	684
Qy	206	PheIlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys	225
Db	685	TTCCAGTTTCAGCAGATCATGAGTGGGCTTATCCCTGGTATATGTCATCTGCTCCGTC	744
Qy	226	TyrCysIleIleIleSerLysLeuSerHisSerLysGlnIleGlnLysArgLysAlaIleu	245
Db	745	TATTGCATTCATCATCTCCAGCTTCACACTCCAAAGGCCACCAAGAGCGCAAGGCTTC	804
Qy	246	LysThrThrValIleleuIleleuAlaPhePheIlaCysTrpLeuProTyrTyrValGly	265
Db	805	AAGACACAGATCATCTCATCTGCGCTTTCGCGCTGTGGCGCTTACTACATATGG	864
Qy	266	IleSerIleAspSerPheIleleuLeuGlyValIleLysGlnGlyCysAspPheGluSer	285
Db	865	ATCAGCATCGACTCTTCATCTCTCTCGGAATAATCATCAAGCAAGGGTGTGATTTGAGAAC	924
Qy	286	IleValHisLysTrpIleSerIleThcGlnAlaIleuAlaPhePheHisCysCysIleuAsn	305
Db	925	ACTGTGCACAGTGGATTTCCATCACCAGGCGCTAGCTTTCTTCACATGTTGTCTGAC	984
Qy	306	ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaIleuAsn	325
Db	985	CCCATCCGTCATGCTTTCCTTGAGAGCCAAATTTAAACCTGTGCCACAGCAGCTACCC	1044
Qy	326	SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgGlyLysHisSer	345
Db	1045	TTCTGTGAGCAGAGGGGTCCAGCCTCAAGATCCTTCCAAAGGAAGAGGAGTGGACATTC	1104
Qy	346	SerValSerThrGluSerGluSerSerSerPheHisSerSer	359
Db	1105	TTCTGTTTCACACTGAGTGTGACTTTCAAAGTTTTCACATCCACG	1146

RESULT 12
 PCT-US94-06380-2
 Sequence 2, Application PC/TUS9406380
 GENERAL INFORMATION:
 APPLICANT: Chuncharapai, Anan
 APPLICANT: Lee, James
 APPLICANT: Hebert, Caroline
 APPLICANT: K. Jin Kim
 APPLICANT: Genentech, Inc.
 TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY DISORDERS
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

1	SOFTWARE: patin (Genentech)		
2	CURRENT APPLICATION DATA:		
3	APPLICATION NUMBER: PCT/US94/06380		
4	FILING DATE:		
5	CLASSIFICATION:		
6	PRIOR APPLICATION DATA:		
7	APPLICATION NUMBER: 08/076093		
8	FILING DATE: 11-JUN-1993		
9	ATTORNEY/AGENT INFORMATION:		
10	NAME: Love, Richard B.		
11	REGISTRATION NUMBER: 34,659		
12	REFERENCE/DOCKET NUMBER: 706622P1		
13	TELECOMMUNICATION INFORMATION:		
14	TELEPHONE: 415/225-5530		
15	TELEFAX: 415/952-9881		
16	TELEX: 910/371-7168		
17	INFORMATION FOR SEO ID NO: 2:		
18	SEQUENCE CHARACTERISTICS:		
19	LENGTH: 1737 bases		
20	TYPE: nucleic acid		
21	STRANDEDNESS: single		
22	TOPOLOGY: linear		
23	PCT-US94-06380-2		
24	Alignment Scores:		
25	Pred. No.: 3.29e-188	Length: 1737	
26	Score: 1678.50	Matches: 319	
27	Percent Similarity: 95.48%	Conservative: 19	
28	Best local Similarity: 90.11%	Mismatches: 11	
29	Query Match: 89.90%	Indels: 5	
30	DB: 5	Gaps: 1	
31	US-09-367-052-2 (1-359) x PCT-US94-06380-2 (1-1737)		
32	QY 6 ValSerIleThrThrSerAspAsnTySerGIuGIuValAlGlySerGlyAspTyrAspSer 25		
33	DB 100 ATTAGTATATACCTTCCTTCAGATTAACACCGAGAAATGGGCTCGAGGAGCTATGACGCC 155		
34	QY 26 AsnLysGIuProCysPheArgAspGIuAsnValLHisPheAsnArgIlePheLeuProThr 45		
35	DB 160 ATGAGGAACCCGCTGTTCCGCTGAGAGAAATGCTAATTCATAAATATCTTCTGCCACC 215		
36	QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGIuAsnGlyLeuValIleLeuValMet 65		
37	DB 220 ATCTACTCCATCATCTTCTTAACTGGCATTTGGGCAATGATGTGTCATCTGTCATG 275		
38	QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysItyrAlaGluLHisLeuSerValAla 85		
39	DB 280 GGTTCACAGAAAGAACTGGAAGCATGACGAGCAAGTACAGGCTCCACCTGTCAGTGGCC 335		
40	QY 86 AspLeuLeuPheValIleThrLeuProPheTrrAlaValAspAlaMetAlaAspTrrTyr 105		
41	DB 340 GACCTCCTCTTTTTCATCAACGCTTCCTCTTGCGCAGTTGATGCGCGTGGCAACTGGTAC 395		
42	QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleItyrThrValAsnLeuTyrSerSer 125		
43	DB 400 TTGGGAACCTCTATGCAAGGACGATGCATCTACACAGTCAACCTGCACAGCAGT 455		
44	QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValLHisAlaThrAsn 145		
45	DB 460 GTCTCTATCCTGGCCCTTCATCAGTCCGACCCCTCACTGGCCATCGTCCACGCCACAC 515		
46	QY 146 SerGIuArgProArgLysLeuLeuAlaGluLysAlaValTyrValGIuValTrrIlePro 165		
47	DB 520 AGTCAGAGGCCAAGAAAGCTGTTGGCTGAAAAAGGTGCTATGTTGGGCTCTGGATCCCT 575		
48	QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185		
49	DB 580 GCCCTCCTGCTGACTTCCTCCGACCTCATCTTTGCCAAGCTC-----AGT 625		
50	QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrrMetValVal 205		
51	DB 625 GAGGACAGTACAGATATATCTGTGTGACCCCTTCACCCCAAGACTTGTGGGTGGTGTG 685		

QY	206	PheGlnPheGlnHisIleMetValGlyLeuIleuProGlyIleValIleLeuSerCys	225
Db	685	TTCCAGTTTCAGCAATCATATGATGGCTTATTCCTGGATGATTTGATCTCTCTCCG	744
QY	226	TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu	245
Db	745	TATTGCATTATCATCTCCAAAGCTGTACACTCCAAAGGCCCAACAGCGCAAGCCCTC	804
QY	246	LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTTPLeuProTyrTyrValGly	265
Db	805	AAGACCAAGCAATCTCATCTGCTTTCCTGGCTTGTGGCTGCTCTACTACTTGGG	864
QY	266	IleSerIleAspSerPheIleLeuLeuGlyIleLysGlnGlyCysAspPheLeuSer	285
Db	865	ATCAGCAATCAAGCTCTTATCTCTCTCGAATTCATCATCAAGCAAGGTGTGACTTTGAGAC	924
QY	286	IleValHisLysTyrPheSerIleThrGlnAlaLeuAlaPhePheHisCysCysLeuAsn	305
Db	925	ACTGTGCACAAAGTGGATTCCATCACCCAGAGCCCTAGCTTTCTTCCACTGTGTGTAAC	984
QY	306	ProIleuThrAlaPheLeuGlnValAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn	325
Db	985	CCCATCTCTATGCTTCTCTTGAGACCCTGTAATTAACCTTGCCCAACAGCATCAACC	1044
QY	326	SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer	345
Db	1045	TCTGTGACACAGAGGGTCCAGCCCTCAAGATCTCTCCAAAGGMAAGCAGGTGCACATTCA	1104
QY	346	SerValSerThrGlnSerGlnSerSerSerPheHisSerSer	359
Db	1105	TCTGTATTCACACTGAGCTGAGTCTTCAAGTTTCACTTCCAC	1146

RESULT 13
 US-08-153-848-45
 Sequence 45, Application US/08153848
 Patent No. 5759804
 GENERAL INFORMATION:
 APPLICANT: Godiske, Ronald
 APPLICANT: Gray, Patrick W.
 APPLICANT: Schmelkart, Vicki L.
 TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSEE: Bicknell
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/153,848
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/977,452
 FILING DATE: 17-NOV-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5759804and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:

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:      LENGTH: 1317 base pairs
:      TYPE: nucleic acid
:      STRANDEDNESS: single
:      TOPOLOGY: linear
:      MOLECULE TYPE: cDNA
:
:      FEATURE:
:      NAME/KEY: CDS
:      LOCATION: 201..1211
:      US-08-153-848-45
:
Alignment Scores:
Pred. No.: 1,11e-11
Score: 1672.50
Percent Similarity: 95.20%
Best Local Similarity: 89.83%
Query Match: 89.58%
DB: 1

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US-09-367-052-2 (1-359) X US-08-153-848-45 (1-1317)

QY	6	ValSerIleLeuThrSerAspAsnIleSerGluValGlySerGlyAspTyrAspSer	25
Db	165	TTCCAGATATACCTTCACATACCTACACCGAGAAATGGGCTCAGGGAGTATAGACTCC	222
QY	26	AsnLysGluProCysPheAsnArgAspGluAsnValHisPheAsnArgIlePheLeuProThr	45
Db	225	ATGAAGAAACCCGTTCCTCGTGAGAAATGCTAATTTCATTAATAATCTCTGCCACC	288
QY	46	IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet	65
Db	285	ATTACTCCATCATCTCTTAACTGGCAATGGGGCAATGGATGGTCATCTGGTCATG	344
QY	66	GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLysSerValAla	85
Db	345	GGTTACCAGAGAAACTGCAAGACATGACGAGCAAGTACAGGCTGCACCTTCAGTGGCC	400
QY	86	AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetValAspTrpTyr	105
Db	405	GACCTCCCTCTTGTCTCATACGCTCCCTCTGGCAGTTGAGGCCGTGGCAAACTGGTAC	464
QY	106	PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer	125
Db	465	TTTGGGAACTCTCTATGCAAGGACATGTCATGATCAACAGTCAACCTCTTACAGAGT	524
QY	126	ValLeuIleLeuAlaPheIleSerLysAspArgTyrLeuAlaIleValHisAlaThrAsn	145
Db	525	GTCTCATCTCGGCTTCATCTACGTGTGAGCCGCTACCTGGCCATCGTCCACGCCAAC	584
QY	146	SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro	165
Db	585	AGTCAGAGGCGCAAGACGTGTGGCTGAAAGGTGGTCTGTGTGGGCTGTGATCCCT	644
QY	166	AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer	185
Db	645	GGCCTCTCTGTGCATTTCCCGACATTCATCTTGGCAACGTC-----AGT	689
QY	186	GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal	205
Db	690	GAGGCAGATGACAGATATATCTGTACCGCTTCTACCCCAATGACTTGTGGGTGTGTG	749
QY	206	PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys	225
Db	750	TTCCAGATTCAGACATCATGTGTGGCTTATCCGCTGGATATTTCATCTCTCTCTCC	809
QY	226	TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu	245
Db	810	TATTCGATTATATCTCCCAAGCTGTGCACACTCCAGAGGCGCACGAGAGCGCAAGCCCTC	869
QY	246	LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly	265
Db	870	AAGACACACAGTATCTCATCTCGCTTTCTTCCGCTGTGGCTGACCTTACTATCATTTGGG	929
QY	266	IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer	285

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Db 930 ATCAGCATGAGCTCTTCATCTCTGGAATCATCAAGAGGTGAGCTTGAGAAC 989
QY 286 ILevalHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 990 ACTGTGCACAGATGATTTCTTCATCAGCGAGCCCTAGCTTCTTCACATGTTGCTGTGAC 1049
QY 306 ProIleLeuTyraIaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 1050 CCCATCCCTATGCTTCTTCCTTGAGAGCCAAATTTAAACCTTGCCACAGCAGCTACAC 1109
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerIleGlyLysArgGlyHisSer 345
Db 1110 TCTGTGACACAGAGGTCCAGCCTCAAGATCCTCTCCAAGGAAAGCGAGGTGAGCATTTCA 1169
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
Db 1170 TCTGTTCCACTGAGTCTGAGTCTTCAAGTTTCACTCCAGC 1211

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Sequence 45, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/320598
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 201..1211

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US-09-299-843A-45
Alignment Scores:
Pred. No.: 1,11e-187 Length: 1317
Score: 1672.50 Matches: 318
Percent Similarity: 95.20% Conservative: 19
Best Local Similarity: 89.83% Mismatches: 12
Query Match: 89.58% Indels: 5
DB: 3 Gaps: 1

US-09-367-052-2 (1-359) x US-09-299-843A-45 (1-1317)
QY 6 ValSerIleTyrrThrSerAspAsnTyrrSerGluGluValGlySerGlyAspTyrrAspSer 25
Db 165 TTGCAGATATACACTCTCATCTGATATACACCGAGAAATGGGCTCAGGGGACTATGACTCC 224
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 225 ATGAAGGAAACCCGTGTTCCGTGAAGAAATGCTAATTTCAATAAATCTTCCTGCCAC 284
QY 46 IleTyrrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 285 ATCTACTCCATCATCTCTTACTGTGGCAATGGAATGGTATCTGCTGCTCATG 344
QY 66 GlyTyrrGlnLysLysLeuArgSerMetThrAspLysTyrrArgLeuHisLeuSerValAla 85
Db 345 GGTATACGAGAAAGAACTAGAAAGCATGACGACAAAGTACAGGCTGCACCTGTGCTGCC 404
QY 86 AspleuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyrr 105
Db 405 GACCTCCTTGTGATCATACACCTTCCCTTGGGAGTTGATGCGGTGCAAACTGTGATC 464
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrrThrValAsnLeuTyrrSerSer 125
Db 465 TTGGGAACCTTCATGCAAGGAGGTGCTATCATCATACAGTCAACCTTACAGCAGT 524
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrrLeuAlaIleValHisAlaThrAsn 145
Db 525 GTCCATCATCTCGGCTTATCATCTGAGCGGTACCTGCGCATCTGACAGCCACAC 584
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrrValGlyValTrpIlePro 165
Db 585 AGTCAGAGCCCAAGAAAGCTGTGGCTGAAAGGTGCTATGTTGGGCTGTGATCCCT 644
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 645 GCCCTCCTGACTATATCCGACTTCACTTGTGCAAGCTC-----AGT 689
QY 186 GlnGlyAspAspArgTyrrIleCysAspArgLeuTyrrProAspSerLeuTrpMetValVal 205
Db 690 GAGGCAGATGACAGATATATCTGTGACCGCTTACCCCATGACTTGTGGTGTGTG 749
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 750 TTCCAGTTTCAAGCATCATGCTGTGGCTTATCCGCTGATGATGATCATCTGCTGC 809
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlnHisGlnLysArgLysAlaLeu 245
Db 810 TATTGCAATTATCATCTCCAGCTGTGACATCTCAAGGCGCACGAAAGCGGAGGCTTC 869
QY 246 LysThrThrValIleLeuIleLeuAlaPheAlaCysTrpPleProTyrrTyrrValGly 265
Db 870 AAGACACAGATCATCTCATCTGCTTCTTCCGCTTGTGGCTGCTTACTACATTGG 929
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db 930 ATCAGCATGAGCTCTTCATCTCTGGAATCATCAAGAGGTGAGCTTGAGAAC 989
QY 286 ILevalHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 990 ACTGTGCACAGATGATTTCTTCATCAGCGAGCCCTAGCTTCTTCACATGTTGCTGTGAC 1049
QY 306 ProIleLeuTyraIaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325

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Db 1050 CCCATCCCTATGCTTCTCTGAGCCAAATTAAACCTGCCGACGACGACTCAC 1109
Qy 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlySerGlyHisSer 345
Db 1110 TCTGTGACCAAGAGGCTCCAGCTCAAGATCTCTCCAAAGAAAGCGAGTGACATTCA 1169
Qy 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
Db 1170 TCTGTTCACCTGAGTGTGAGTCTTCAAGTTTTCACCTCCAGC 1211

RESULT 15

US-09-088-337B-45
Sequence 45, Application US/09088337B
Patent No. 6348574

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-0448
TELEFAX: (312) 474-6300

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

NAME/KEY: CDS
LOCATION: 201..1211
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-088-337B-45

Alignment Scores:

Pred. No.: 1,11e-187 Length: 1317
Score: 1672.50 Matches: 318
Percent Similarity: 95.20% Conservative: 19
Best Local Similarity: 89.83% Mismatches: 12
Query Match: 89.58% Indels: 5
DB: 4 Gaps: 1

US-09-367-052-2 (1-359) x US-09-088-337B-45 (1-1317)

Qy 6 ValSerIleYrThrSerAspAsnTyrSerGluIleValGlySerGlyAspTyrAspSer 25
Db 165 TTGCAGATATATACCTTTCAGATTAATACACCGAGAAATGGGCTCAGGAGACTATGATCC 224
Qy 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 225 ATGAAGAGAACCCCTTTCCGCGAAGAAATGCTTAATTAATAAATCTCTGCCACC 284
Qy 46 IleYrThrIleIlePheLeuThrClyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 285 ATCTACTCCATCATCTTTTAACCTGCAATGTCGCAATGATGATTCATCTCGGTATG 344
Qy 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 345 GGTTCACCAAGAAAGACTGAGAGATACGACGACAGATACAGGCTGCACCTGTGATGCC 404
Qy 86 AspleuLeuPheValIleThrLeuProPheThrPalValAlaMetAlaAspTrpTyr 105
Db 405 GACCTCCTCTTGTATCAGACGCTTCCCTCTGCGAGATGTGATGCGCGCAAACTGGTAC 464
Qy 106 PheGlyLysPheLeuCysLysAlaValHisIleIleYrThrValAsnLeuTyrSerSer 125
Db 465 TTGGAAGACTTCATATCCAGAGCAGTCATGTCATACACAGTCAACCTCTACAGAGT 524
Qy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 525 GTCCATATCCGGGCTTCATCATGCTGACGACCGCTACCTGGCCATCGCCACGACAC 584
Qy 146 SerGlnArgProArgLysLeuLeuAlaGlyLysAlaValYrValGlyValTrpIlePro 165
Db 585 AGTCAGAGGCCAAGAGAGCTGTGGCTGAAGAGGTGCTATGTTGGCGTCTGATCCCT 644
Qy 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 645 GCCCTCTGCTGACTATTCGCGACTCATCTTGGCCACGTC-----AGT 689
Qy 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValAla 205
Db 690 GAGGACAGATGACATATATCTGACGCGCTTACCCCAATGATCTGTGGTGTGTG 749
Qy 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 750 TTCAGATTTCAGCATCATGATGTTGGCTTATCTGCTGATATTCATCTGTCTCTCC 809
Qy 226 TyrGlyIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 810 TATTGCAATTATCATCTCCAGCTGTCACACTCCAAAGGCCACCGAAGCGAAGGCCCTC 869
Qy 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
Db 870 AAGACACAGATCACCTCATCTGCTTCTGCGCTGTGGCTTACTACTACTGATGGG 929
Qy 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db 930 ATCAGCATCGACTCTTCATCTCTCTGGAATATCATCAAGCAAGGCTGTGAGTGAAG 989
Qy 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysLysLeuAsn 305
Db 990 ACTGTGACAGATGATTCATCTACACGAGGCCCTACTCTTCTTCCACTGTGTGTAAC 1049
Qy 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 1050 CCCATCCCTATGCTTCTCTGAGCCAAATTAAACCTCTGCCGACGACGACTCAC 1109
Qy 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlySerGlyHisSer 345
Db 1110 TCTGTGACCAAGAGGCTCCAGCTCAAGATCTCTCCAAAGAAAGCGAGTGACATTCA 1169
Qy 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
Db 1170 TCTGTTCACCTGAGTGTGAGTCTTCAAGTTTTCACCTCCAGC 1211

Mon Jul 14 09:29:48 2003

us-09-367-052-2.rni

Page 15

Search completed: July 12, 2003, 18:12:29
Job time : 67 secs

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GenCore version 5.1.6
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OW protein - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 17:51:24 : Search time 155 Seconds
(without alignments)
3657.157 Million cell updates/sec

Title: US-09-367-052-2

Perfect score: 1867

Sequence: 1 MERISIVSYSDNVSEVGS.....KRGHSSVSNESSESPFSS 359

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1105431 segs, 789497651 residues

Total number of hits satisfying chosen parameters: 2210862

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool/US09367052/runat_10072003_100047_10536/app_query.fasta.1.519
-DB=published.Applications_NA -OFMT=fastap -SUFFIX=trnp -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US9367052.ecgn_1_125_etrunat_10072003_100047_10536
-NCPU=6 -ICPU=3 -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELLOCK=100
-LONGLOG -DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:

1: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/Pct_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1678.5	89.9	1670	US-09-880-107-2143	Sequence 2143, Ap
2	1678.5	89.9	1679	US-10-225-567A-75	Sequence 75, Appl
3	1678.5	89.9	1737	US-09-104-063-3	Sequence 3, Appl
4	1670.5	89.5	1102	US-09-870-759-143	Sequence 143, App

5	1139	61.0	1902	US-09-953-692-1	Sequence 1, Appl
6	1139	61.0	1902	US-09-953-717-1	Sequence 1, Appl
7	657.5	35.2	421	US-09-796-682-2611	Sequence 2611, Ap
8	657.5	35.2	421	US-10-040-862-2611	Sequence 2611, Ap
9	584	31.3	1107	US-10-251-385-19	Sequence 19, Appl
10	584	31.3	1670	US-10-225-567A-73	Sequence 73, Appl
11	584	31.3	1670	US-09-880-107-3833	Sequence 3833, Ap
12	580	31.1	1107	US-10-251-385-173	Sequence 173, Ap
13	575	30.8	1877	US-10-106-688-2125	Sequence 125, Ap
14	570.5	30.6	1607	US-10-120-394-19	Sequence 19, Appl
15	570.5	30.6	1607	US-09-764-413-19	Sequence 19, Appl
16	570.5	30.6	1677	US-10-225-567A-65	Sequence 65, Appl
17	570.5	30.6	1677	US-09-837-446-1	Sequence 1, Appl
18	555	29.7	1068	US-10-237-563-47	Sequence 47, Appl
19	552	29.6	1068	US-10-237-563-48	Sequence 48, Appl
20	549.5	29.4	1068	US-10-237-563-41	Sequence 41, Appl
21	549.5	29.4	1068	US-10-237-563-43	Sequence 43, Appl
22	549	29.4	1068	US-10-237-563-42	Sequence 42, Appl
23	546	29.2	1068	US-10-237-563-45	Sequence 45, Appl
24	544.5	29.2	1068	US-10-237-563-38	Sequence 38, Appl
25	544.5	29.2	1068	US-10-237-563-39	Sequence 39, Appl
26	544.5	29.2	1068	US-10-225-567A-385	Sequence 46, Appl
27	543.5	29.1	1053	US-10-237-563-46	Sequence 46, Appl
28	542.5	29.1	1053	US-10-237-563-40	Sequence 40, Appl
29	541.5	29.0	1068	US-10-237-563-44	Sequence 44, Appl
30	540	28.9	1487	US-10-225-567A-248	Sequence 248, App
31	540	28.9	1487	US-09-789-482-3	Sequence 3, Appl
32	540	28.9	1487	US-09-789-486-3	Sequence 1, Appl
33	540	28.9	3100	US-10-290-058A-1	Sequence 267, App
34	540	28.9	3100	US-09-954-456-267	Sequence 267, App
35	540	28.9	3100	US-09-954-456-945	Sequence 1588, Ap
36	540	28.9	3100	US-09-954-456-1588	Sequence 73, Appl
37	537.5	28.8	1137	US-10-251-385-73	Sequence 289, App
38	537.5	28.8	2139	US-10-225-567A-67	Sequence 23, Appl
39	535	28.7	2100	US-10-313-542-89	Sequence 240, App
40	534	28.6	1074	US-10-251-385-23	Sequence 1, Appl
41	534	28.6	2462	US-10-225-567A-240	Sequence 1, Appl
42	534	28.6	2577	US-09-966-755-1	Sequence 1, Appl
43	534	28.6	2577	US-09-963-377-1	Sequence 1, Appl
44	534	28.6	2577	US-09-932-385-1	Sequence 1, Appl
45	534	28.6	2577	US-10-000-759A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-880-107-2143
Sequence 2143, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darcil T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2143
LENGTH: 1670
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 L06797
US-09-880-107-2143
Alignment Scores:

Pred. No.: 3,31e-182 Length: 1670
 Score: 1678.50 Matches: 319
 Percent Similarity: 95.48% Conservative: 19
 Best Local Similarity: 90.11% Mismatches: 11
 Query Match: 89.90% Indels: 5
 Gaps: 1

US-09-367-052-2 (1-359) x US-09-880-107-2143 (1-1670)

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Qy 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValAlaGlySerGlyAspTyrAspSer 25
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Qy 26 AsnysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 142 ATGAGAGAACCCCTTTCCGGAAGAAATGCTTAATTCATATAAATCTTCTCCACC 201
Qy 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 202 ATCTACTCCATCATCTTCTTAACTGGCATTTGCGCATGATGGTGCATCCCTGTCATG 261
Qy 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 262 GGTTCACGAGAAAGAACTGAGAGCATGACGACAAAGTACAGGCTGCACCTGTCACTGCC 321
Qy 86 AspleuLeuPheValIleThrLeuProPheTyrPheValAlaAspAlaMetAlaAspTyr 105
Db 322 GACCTCCTCTTTGTCATCAGCCCTTCCCTTGGGCACTGTATGCGCGGCAAACTGGTAC 381
Qy 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 382 TTTGGCACTTCCATCAAGGAGCTCAAGTCACTCAACAGTCAACCTTACAGCAGT 441
Qy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 442 GTCTCTACCTCGGCTTCATAGTCTGACCGCTACCTGGGCACTGTCACGACGACCAAC 501
Qy 146 SerGlnArgProArgLysLeuAlaGluLysAlaValTyrValGlyValTyrPhePro 165
Db 502 AGTCAGAGGCCAAGAGAGCTGTGGCTGAAGAGTGTCTATGTGGGCTGTGATCCT 561
Qy 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 562 GCCCTCTGCTGACTATTCGCCGACTCATCTTCCCAACGAC-----AGT 606
Qy 186 GlnGlyAspAspArgTyrIleCysAspArgTyrProAspSerLeuTyrPheValVal 205
Db 607 GAGGCAATGACATATATCTGTGACCGCTTCAACCCAAATGACTTGTGGGTGTGTG 666
Qy 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 667 TTCAGATTTCAGACATCATGTTGGCTTATCTGCGTGTATTTGCATCTCTCTCGC 726
Qy 226 TyrTyrIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysAlaGlyAlaLeu 245
Db 727 TATTGCAATTATCATCTCAACCTGTCAACACCAAGGCCACGAAGCGGAGCCCTC 786
Qy 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrPheProTyrTyrValGly 265
Db 787 AAGACCAAGTCACTCTCATCTGCTTCTTCCGCTGTGGCTTACTTAATTTGGG 846
Qy 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db 847 ATCAGCATCGACTCTTCATCTCTCTGGAATCATCAAGCAAGGCTGTGAGATTGAGAC 906
Qy 286 IleValHisLysTyrPheSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
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Qy 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
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Qy 326 SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyAsnArgGlyHisSer 345
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 Db 1087 TCTGTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCAGC 1128

RESULT 2

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US-10-225-567A-75
: Sequence 75, Application US/10225567A
: Publication No. US20030113798A1
: GENERAL INFORMATION:
: APPLICANT: Lifespan Biosciences
: APPLICANT: Brown, Joseph P.
: APPLICANT: Burner, Glenn C.
: APPLICANT: Roush, Christine L.
: TITLE OR INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
: FILE REFERENCE: 1920-4-4
: CURRENT APPLICATION NUMBER: US/10/225,567A
: PRIOR FILING DATE: 2001-12-19
: PRIOR APPLICATION NUMBER: 60/257,144
: NUMBER OF SEQ ID NOS: 292
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 75
: LENGTH: 1679
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-225-567A-75

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Alignment Scores:

Pred. No.: 3,33e-182 Length: 1679
 Score: 1678.50 Matches: 319
 Percent Similarity: 95.48% Conservative: 19
 Best Local Similarity: 90.11% Mismatches: 11
 Query Match: 89.90% Indels: 5
 Gaps: 1

US-09-367-052-2 (1-359) x US-10-225-567A-75 (1-1679)

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Qy 26 AsnysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 158 ATGAGAGAACCCCTTTCCGGAAGAAATGCTTAATTCATATAAATCTTCTCCACC 217
Qy 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 218 ATCTACTCCATCATCTTCTTAACTGGCATTTGCGCATGATGGTGCATCCCTGTCATG 277
Qy 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 278 GGTTCACGAGAAAGAACTGAGAGCATGACGACAAAGTACAGGCTGCACCTGTGAGCC 337
Qy 86 AspleuLeuPheValIleThrLeuProPheTyrPheValAlaAspAlaMetAlaAspTyr 105
Db 338 GACCTCCTCTTTGTCATCAGCCCTTCCCTTGGGCACTGTATGCGCGGCAAACTGGTAC 397
Qy 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 398 TTTGGCACTTCCATATCAGGAGCTGTCAATGTATCAACAGTCAACACTCTACAGCAGT 457
Qy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 458 GTCTCTACCTCGGCTTCATAGTCTGACCGCTACCTGGGCACTGTCACAGCAGCAGCAAC 517
Qy 146 SerGlnArgProArgLysLeuAlaGluLysAlaValTyrValGlyValTyrPhePro 165
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Oy 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaIleValSerGlnGlyAspIleSer 185
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Oy 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
Db 623 GAGCAGATGACAGATATATCTTGACCGGCTTACCCCAATGACATGACTGTGGGTGGTGTG 682
Oy 206 PheIleIlePheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 683 TTCCAGTTTCAGCAGATCATAGTGGGCTTAATCCGCTGGTATGATTCATCTCTCCGTC 742
Oy 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlnHisGlnLysArgLysAlaLeu 245
Db 743 TATTCGATATATCATCTCCAGCTTCACACTCCAGAGGCCACAGAACGCCAAGGCCCTC 802
Oy 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
Db 803 AAGACACAGCATCATCCATCTCTGGCTTCTCCGCTGGTGGCGCTTATCATATGGG 862
Oy 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
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Oy 286 IleValHisLysTrpIleSerIleThrGlnAlaLeuAlaPhePheHisCysCysLeuAsn 305
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Oy 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
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Oy 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
Db 1043 TCTGTGAGCAAGAGGCTCAGGCTCAAGATCTCTCCAAAGSAAAGCCAGGTGACATTCA 1102
Oy 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
Db 1103 TCTGTTCCACTGAGTCTGAGTCTTCAAGTTTCCACTCCACG 1144

RESULT 3
US-09-104-063-3
: Sequence 3, Application US/09104063
: Patent No. US20020168356A1
: GENERAL INFORMATION:
: APPLICANT: Lee, James
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: PRAA Receptors
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Geneentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Geneotech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/104,063
: FILING DATE: 24-June-1998
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/701265
: FILING DATE: 22-AUG-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/664228
: FILING DATE: 06-JUN-1996
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 08/076093

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	FILEIN DATE: 11-JUN-1993	
	PRIOR APPLICATION DATA: 07/810782	
	APPLICATION NUMBER: 07/810782	
	FILING DATE: 19-DEC-1991	
	ATTORNEY/AGENT INFORMATION:	
	NAME: Love, Richard B.	
	REGISTRATION NUMBER: 34,659	
	REFERENCE/DOCKET NUMBER: P0706P2C2	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: 415/225-5530	
	TELEFAX: 415/952-9881	
	TELEX: 910/371-7168	
	INFORMATION FOR SEQ. ID NO: 3:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 1737 base pairs	
	TYPE: Nucleic Acid	
	STRANDEDNESS: Single	
	TOPOLOGY: Linear	
	US-09-104-063-3	
	Alignment Scores:	
	Pred. No.: 3,52e-182	
	Score: 1678.50	
	Percent Similarity: 95.48%	
	Best Local Similarity: 90.11%	
	Query Match: 89.90%	
	DB: 9 Gaps: 1	
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DB	100 ATCAGTATATACACTTCAGATACTACACCGAGAAATGGGCTGAGGGAGCTATGACTCC	159
QY	26 AsnLysGluPProCysShearGaspGluAsnValHisPheAsnAArgllePheLeuPProThr	45
DB	160 ATGAGAGAACCCGTTTCCGTCAGAGAAATGCTAATTTTCATTAATAATCTTCCGCCACC	219
QY	46 lleTYrPhelellePheLeuThrGlylleValaGlyAsnGlyLeuValilleLeuValMet	65
DB	220 ATCTACTCCATCATCTTCTTACTGTGCATTTGGGCAATGGATTTGGTATCTCTGTCATG	279
QY	66 GlyTYrGlnLysLysLeuArgSerMetThrAspLysTYrATrGLeuHisLysLeuSerVala	85
DB	280 GGTACACAGAAAGAACTGAGAAAGCATGACGGACAAGTACAGAGCTGACACTGTCAGTGGCC	339
QY	86 AspLeuLeuPheValilleThrLeuPProPheTrpAlaValaAspAlaMetAlaAspTrpTYr	105
DB	340 GACCTCTCTTGTTCATCACGCTCCCTTCTGGGAGTGTGATGCCGTGGCAAACTGGTAC	399
QY	106 PheGlyLysPheLeuLysLysAlaValaHisillelleTYrThValAsnLeuTYrSerSer	125
DB	400 TTTGGGAATCTCTATGCAAGGAGCCATGTCATCTACACAGTCACCTCTACAGCAGT	455
QY	126 ValLeuilleLeuAlaPheIleSerLeuAspArgTYrLeuAlaIleValaHisAlaThrAsn	145
DB	460 GTCTCTATCTGTGACTTCATCAGTGGAGCCCTTACTGGCCATTCGTCACGCCACCAAC	519
QY	146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValaTYrValaGlyValTrpIlePro	165
DB	520 AGTCAGAGGCGCAAGGAAGCTTTGGCTGAAAAGTGTCATGTTGGGCTGTGATCCCT	579
QY	166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer	185
DB	580 GCCCTCTCTGTGACTTTCGCCGACTTCATCTTGGCAACGTC-----AGT	624
QY	186 GlnGlyAspAspArgTYrIleCysAspArgLeuTYrProAspSerLeuTrpMetValaVal	205
DB	625 GAGGCAATATCAAGATATATCTGTGACCCCTTCTACCCCAATGACTTGTGGGTGGTGTG	684
QY	206 PheGlnPheGlnHisIleMetValaGlyLeuIleLeuProGlyIleValaIleLeuSerCys	225
DB	685 TTCACAGTTTACGACATTCATGTTGGCTTATCTTCGCTGGATATGTCATCTCTCTGCG	744


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PRIOR APPLICATION NUMBER: 09/358,624
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: 60/093,596
PRIOR FILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1902
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: unsure
LOCATION: (158) (223) (225) (226) (335) (466) (520) (530) (645) (763) (825) (1120)
LOCATION: (1183)
US-09-953-692-1

Alignment Scores:
Pred. No.: 2,71e-120 Length: 1902
Score: 1139.00 Matches: 307
Percent Similarity: 75.41% Conservative: 18
Local Similarity: 71.23% Mismatches: 23
Identity Match: 61.01% Indels: 88
Gaps: 21

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Db 103 AGTATATACACTTTCGATACACTACACCGAAGAAATGGGCTCAGGGGACATA-SYTSNDNYTM 161
OY 24 -----AspSerAsnLysGluProCysPheArgAspGluAsnValHisPheAsn----- 39
Db 162 GSGDYTAGCTCCATGAAGAACCCCTGTTCCGTGAAGAAATGCTAATTCATADSMKC 221
OY 40 -----ArgIlePheLeuProThrIleTyrPheIleIlePheLeuThrGlyIleVal----- 56
Db 222 RNANNAATCTCTCCGCCCCACCATCTACTCCATCTCTTCACTGCGATTGTGTYST 281
OY 57 --GlyAsnGlyLeuValIleLeuValMetGlyTyrGlyLysLysLeuArg----- 72
Db 282 GVGGAATGGATGGTGCATCCCTGGTCATGGGTTACCAGAGAACTGAGAGAGNGVWGY 341
OY 73 --SerMetThrAspLysTyrArgLeuHisLeuSerValAlaLysPheLeuPheVal----- 90
Db 342 KKRSCATGACGGACAGTACAGCTGCACCTGTCACTGGCCGACCTCTTGM-TDKY 400
OY 91 -----IleThrLeuProPheTrpPalaValAspAlaMetLysAspTrpTyrPhe----- 106
Db 401 RHSVADTCATCAGCTTCCCTTCTGGGCGAGTGTGATGCGCGTGCACAACTGGTACTTTVWA 460
OY 107 -----GlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeu----- 122
Db 461 VDAVANWVGGAACACTTCCATCCAAAGCGCATGCTACTACACAGTCAACCTCTAGN 520
OY 123 -----TyrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAla 139
Db 521 CKAHVHTVNCACAGCTGCTCTCATCCGCGCTTCATCAGTGCAGCGTACCTACCGGCG 580
OY 140 -----IleValHisAlaThrAsnSerGlnArgProArgLysLeuLeuAlaGluLys 156
Db 581 ASSVASDRATCTGTCAGCGCCCAACAGTCCAGAGGCCCAAGAACCTGTGGCTGAAAG 640
OY 157 Ala-----ValTyrValGlyValTrpIleProAlaLeuLeuThrIle--Pr 172
Db 641 VHT-ATNSRRKAKGTGTCTATGTGGCGTCTGATCCCTGCTCTGCTGACTATTC 699
OY 172 O-----AspPheIlePheAlaAspValSerGlnLysAspIleSerGlnGlyAspAs 189
Db 700 GAVVTVGVWATDCTTCATCTTGGCAAGCTC-----AGTGGACGACGATGA 744
OY 189 parGrTyrIleCysAspArg-----LeuTyrProAspSerLeuTyrMetValVa 205
Db 745 CAGATATATCTGTGACCA-NVSADRDYCDGCTTCTACCCCAATGACTGTGGTGTCT 803
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OY 205 lPheGlnPheGlnHisIle-----MetValGlyLeuIleLeuProGlyIleValI1 222
Db 804 GTTCCAGTTTCAGCACATCRNYDMWVYHATGGTTGGCTTATCCGCGCTGATGTCTAT 863
OY 222 eLeuSerCysTyrCysIle-----IleIleSerLysLeuSerHisSerLysGlyH1 239
Db 864 CCTGTCTCTCATTTGCATWGVSCVCTATCTCAAGCTGTCACTCACTCCAGGGCCA 923
OY 239 sGlnLysArgLysAla-----LeuLysThrTrpValIleLeuIleLeuAlaPhe 255
Db 924 CCAGAAAGCGCAAGGCCSKSHSKGHRKRATCAAGACACAGTCACTCATCTGCTT 983
OY 255 ePheAlaCysTrpLeuPro-----TyrTrpValGlyIleSerIleAspSerPheIle 272
Db 984 CTTCGCGCTTGGCTGCCCTKRTTVAACWPTACTCATTTGGATAGCATGCATCTTCAATC 1043
OY 273 LeuLeuGlyValIleLys-----GlnGlyCysAspPheGluSerIleValHisLysTr 290
Db 1044 CTCTCGAANAATCATCAAAAYGSDSKGCACAGGCGTGTGAGAACACTGTGCACAGTG 1103
OY 290 PlleSerIleThr-----Glu-AlaLeuAlaPhePheHisCysCysLeuAsnProI 307
Db 1104 GATTTCCATCACCGCGCNTVHKWSTAGGCCCTTCTTCCACGTGTGTGAACCCCA 1163
OY 307 lLeuTyrAlaPhe-----LeuGlyAlaLysPheLysSerSerAlaGlnHisAlaL 324
Db 1164 TCTCTATATGC-TTTCAHACCNACTTTGGAGCCAAATTTAAACCTTGCGCCACGACGC 1222
OY 324 eAsnSerMet-----SerArgLysSerSerLeuLysIleLeuSerLysGly 339
Db 1223 TCACCTCTTGGAGGAKRTSAHATSVSCAGAGGCTCAGGCTCAAGATCTCTCCAAAGA 1282
OY 340 LysArgGlyGlyHis-----SerSerValSerThrGluSerGluSerSerSe 355
Db 1283 AAGCAGAGTGAGCATTTGSSSKSGKRGHCATCTGTTCCACTGAGTGTGAGTCTTCAAG 1342
OY 355 rPheHisSerSer 359
Db 1343 TTTTCACTCCAGC 1355

RESULT 6
US-09-953-717-1
; Sequence 1, Application US/09953717
; Patent No. US20020107196A1
; GENERAL INFORMATION:
; APPLICANT: Shalley, Gupta K.
; TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by
; FILE REFERENCE: P50676D1
; CURRENT APPLICATION NUMBER: US/09/953,717
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 09/358,624
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/093,596
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1902
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: unsure
LOCATION: (158) (223) (225) (226) (335) (466) (520) (530) (645) (763) (825) (1120)
LOCATION: (1183)
US-09-953-717-1

Alignment Scores:
Pred. No.: 2,71e-120 Length: 1902
Score: 1139.00 Matches: 307
Percent Similarity: 75.41% Conservative: 18
Best Local Similarity: 71.23% Mismatches: 23
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Query Match:	61.01%	Indels:	88
DB:	10	Gaps:	21

QY	7	SerIleYrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyr-----	23
Db	103	AGTATATACACTCTCGATTAAGTACACAGGAAATGGGCTCAGGGGACTA-SYTSNDNYTM	161
QY	24	-----AspSerAsnLysGluProCysPheArgAspGluAsnValHisPheSer-----	39
Db	152	GSQDTGACATCCATAGAAAGAACCCCTGTTCCGTGAAGAAATGCAATTTCAATTDMSKC	221
QY	40	----ArgIlePheLeuProThrIleTyrPheIleIlePheLeuThrGlyIleVal-----	56
Db	222	RNANNAATCTCTCCGCCACACTACTCATCTCTCTTAATCGCATATGTGKTST	281
QY	57	--GlyAsnGluLeuValIleLeuValIleMetGlyTyrGlnLysIleuArg-----	72
Db	282	GVGGCAATGAGATTGGTCTCATCTCGGTCATGGGTTACCAAGAACTGAGAAAGNGVWGK	341
QY	73	--SerMetThrAspLysTyrArgLeuHisIleSerSerValAlaAspLeuPheVal-----	90
Db	342	KKRSCTATGACGGACAAAGTAAAGCGTCGACCTGTAGTGGCGGACCTCCTCTTGM-TDKY	400
QY	91	-----IleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyrPhe----	106
Db	401	RHSVADTCATACGCTCTCCCTTGGGAGTTGATGACGCTGGCAACGAGTACTTTWMA	460
QY	107	-----GlyLysPheLeuGlyLysAlaValHisIleIleTyrThrValAsnLeu----	122
Db	461	VDAAVAMWGGGAACTTCTCTATGCAAGGACGATCATGTATCTACACAGTCAACCTCTG	520
QY	123	-----TyrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAla	139
Db	521	CKAVHYTVNVCACGAGCTGCTCTCATCTCGGCTTCATCAGCTGAGCGGTACTGCGCC	580
QY	140	-----IleValHisAlaThrSerGlnArgProArgLysLeuLeuAlaGluLys	156
Db	561	ASSVASDRATGCTGACGACCAACAGTCAAGAGGCCAAGAAAGCTGTGGCTGAAG	640
QY	157	Ala-----ValTyrValGlyValTrpIleProAlaLeuLeuLeuThrIle-Pr	172
Db	641	VH-ATNSRKAKKAGTGCTGATGGTGGCTGCGATCCCGCTCTGCTGATCTTCC	699
QY	172	O-----AspPheIlePheAlaAspValSerGlnLysPheIleSerGlnLysAsp	189
Db	700	GAVVYGVWANDCTTCATCTTGCCACAGTC-----AGTGGCGAGATGA	744
QY	189	ParGlyrIleCysAspArg-----LeuThrProAspSerLeuTrpMetValVa	205
Db	745	CAGATATATCTGTGACCA-NVSADRYDGGCTTCAACCCAAATGACTGTGGGTGGTGT	803
QY	205	IleGlnIleGlnHisIle-----MetValGlyLeuIleLeuProGlyIleValI	222
Db	804	GTTCCAGTTTCAGCACAATCRNMDVWVHATGGTGGCTTATCTCGCTGATGTGAT	863
QY	222	eleuSerCysTyrCysIle-----IleIleSerLysIleuSerHisSerLysGlyHi	239
Db	864	CCTGTCTCCATATTCATMWGVSCTYATATCTCCCAAGCTGTCCACTCCAAAGGCCA	923
QY	239	SGlnLysArgLysAla-----LeuLysThrThrValIleLeuIleLeuAlaPh	255
Db	924	CCAGAGGCGCAGGCGCCSKSHKRRATCAAGACCAAGATCACTCTCATCTGGCTTT	983
QY	255	ePheAlaCysTrpLeuPro-----TyrTyrValGlyIleSerIleAspSerPheIle	272
Db	984	CTTCGCTGTGGCGCCTKTTVACWMTACTACATTGGGATCAGCATGACTCTTATC	1044
QY	273	LeuLeuGlyValIleLys-----GlnGlyCysAspPheGluSerIleValHisLysTr	290
Db	1044	CTCCCGGAATCATCAATAAVYSDSKCAAGGCGTGTAGTTTGGAACACTGTGGCAAAAGT	1103

QY	230	PILeSerIlethr-----	GLu-AlaLeuAlaPhePheHisCysCysLeuAnsProI	307
Db	1104	GATTTCCATCCACCGGCNTVHKMSTAGAGCCCTTTTCTTCACATGGTGTGGAACCCCA		1163
QY	307	IeIeuTyfAlaPhe-----	LeuGlyAlaIysPheIysSerSerAlaGlnHisAlaI	324
Db	1164	TCCTCTATAGC--TTTCAHCCNACTTGGAGGCCAAATTTAAAAACCTCTGCCAGCAGCCAC		1222
QY	324	euaAnsSerMet-----	serArgGlySerSerIleuLysIleLeuSerIysGly	339
Db	1223	TCACCTCTGTGAGGAKKTSANATVSCAGAGGGTCCACGCTTCACAAAGGA		1288
QY	340	LysArgGlyGlyLynHis-----	SerSerValSerThrGlnSerGluSerSerSer	355
Db	1283	AAGCAGAGTGAGCATTRRSSKSKGRGGHCATCTGTTCCACTGAGTGTGAGGTCTTCAAG		1344
QY	355	rPheHisSerSer	359	
Db	1343	TTTTTCACATCCAGC	1355	

RESULT 7

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US-09-796-6922611
; Sequence 2611, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
; FILE OF INVENTION: HISTOPATHOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796.692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: fastseq for Windows Version 3.0
; SEQ ID NO 2611
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-2611

Alignment Scores:
Pred. No.: 3,91e-66 Length: 421
Score: 657.50 Matches: 125
Percent Similarity: 92.36% Conservative: 8
Best Local Similarity: 86.81% Mismatches: 5
Query Match: 35.22% Indels: 5
DB: 9
Gaps: 1

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ORGANISM: Homo sapiens
us-10-251-385-19

Alignment Scores:
Pred. No.: 4,65e-57 Length: 1107
Score: 584.00 Matches: 124
Percent Similarity: 54.26% Conservative: 67
Best Local Similarity: 35.23% Mismatches: 139
Query Match: 31.28% Indels: 22
DB: Gaps: 5

US-09-367-052-2 (1-359) x US-10-251-385-19 (1-1107)

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QY 12 AspAsnTYRserGluValAlGlyserGlyAspTYRAspSerAsn-----Lys 27
DB 61 GAGAACTTCAGCTCTTCTATGACTATGAGAAAAGAGAGTACTGCTGCTGTAACCTCC 120
QY 28 GluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyr 47
DB 121 CCGGCTCCGACAGAGACTTCAAGCTGAACTTCAGCCGGGCTTCCTCCAGCCCTCTAC 180
QY 48 PheIleIlePheLeuThyGlyIleValAlGlysnGlyLeuValIleLeuValMetClyTyr 67
DB 181 AGCCCTCTCTTCTGCTGGGCTGCTGGCAAGCGGGGGGAGCCGCTGCTGTAGC 240
QY 68 GluLysLysLeuArgSerMetThrAspLysTYRArgLeuHisLeuSerValAlaAspLeu 87
DB 241 CCGCGGACAGCCCTGAGCAGCAGCAGCAGCTTCTGCTCCAGCTGAGCTGAGCAGCAGC 300
QY 88 LeuPheValIleThrLeuProPheThrAlaValAlaAspAlaMetAlaAspTrpTyrPheGly 107
DB 301 CTGCTGAGTGTACACTGCGCTGCGGAGAGGAGCTGCGCTGAGTGTCTTTGGC 360
QY 108 LysPheLeuGlyLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeu 127
DB 361 TCTGCCCTCTGCAAGTGGGAGGAGGCTGCTTCAACATCAACTTCTAGCAGAGAGCCCTC 420
QY 128 IleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsnSerGln 147
DB 421 CTGCTGCGCTGATCATGACTTTGACCGCTACCTGACATAGTTCATGACCCAGCTGAC 480
QY 148 ArgProArgLysLeuLeuAlaGlyLysAlaValTyrValGlyValTyrIleProAlaLeu 167
DB 481 CCGCGGGGGGCGCGCGCGCTGACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 168 LeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSerGlnGly 187
DB 541 CTTTTGGCTCCCAAGACTTCACTTCTGCTG-----GCCACACAC 582
QY 188 AspAspArgTyr-----IleCysAspArgLeuTyrProAspSerLeuTrpMetVal 204
DB 583 GACGAGCGGCTCAAGCCGACCCAGCAGCAGTCAACTGCCA---CAGTGGGCGGACAG 639
QY 205 ValPheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSer 224
DB 640 GCTCTGCGGGTCTGCTGAGCTGGTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 699
QY 225 CysTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAla 244
DB 700 TGTATGCCCCACATCTGCGCGCTGCTGCTGCTTCCAGGGGAGGAGGGGCTGCGGGGCT 759
QY 245 LeuLysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrVal 264
DB 760 ATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 819
QY 265 GlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGlu 284
DB 820 GTGGTCTGCTGAGCATCTCATGAGCTGGGCGCTTTGGCCCAACTGTGGCCAGAG 879
QY 285 SerIleValHisLysTrpIleSerIleThrGlnAlaLeuAlaPheHisLysCysGln 304
DB 880 AGCAGGAGTAGAGCTGGCCAAAGTCGCTACCTCAGGCGCTGGGCTGACATGACCTGCTCC 939

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QY 305 AsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeu 324
DB 940 AACCCCTGCTATGCTTGTAGGGGTGATCCGAGAGGAGATGATGATGCTGCTC 999
QY 325 AsnSerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlnHis 344
DB 1000 -----TTCGGCTGGGCTGCCCAACAGAGAGGGCTCCAG 1035
QY 345 SerSerValSerThrGlnSerGlnSerSerPhe 356
DB 1036 AGCAGCCATCGCTTCCCGGGGATTCATCTCG 1071

RESULT 10
US-10-225-567A-73
; Sequence 73, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225, 567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 1670
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-225-567A-73

Alignment Scores:
Pred. No.: 8.82e-57 Length: 1670
Score: 584.00 Matches: 124
Percent Similarity: 54.26% Conservative: 67
Best Local Similarity: 35.23% Mismatches: 139
Query Match: 31.28% Indels: 22
DB: Gaps: 5

US-09-367-052-2 (1-359) x US-10-225-567A-73 (1-1670)
QY 12 AspAsnTYRserGluValAlGlyserGlyAspTYRAspSerAsn-----Lys 27
DB 129 GAGAACTTCAGCTCTTCTATGACTATGAGAAAAGAGAGTACTGCTGCTGTAACCTCC 188
QY 28 GluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyr 47
DB 189 CCGGCTCCGACAGAGACTTCAAGCTGAACTTCAGCCGGGCTTCCTCCAGCCCTCTAC 248
QY 48 PheIleIlePheLeuThyGlyIleValAlGlysnGlyLeuValIleLeuValMetClyTyr 67
DB 249 ACCCTCTCTTCTGCTGGGCTGCTGGGCAAGCGGGGTGGAGCGGCTGCTGAGC 308
QY 68 GluLysLysLeuArgSerMetThrAspLysTYRArgLeuHisLeuSerValAlaAspLeu 87
DB 309 CCGCGGACAGCCCTGAGCAGCAGCAGCAGCTTCTGCTCCAGCTGAGCTGAGCAGCAGC 368
QY 88 LeuPheValIleThrLeuProPheThrAlaValAlaAspAlaMetAlaAspTrpTyrPheGly 107
DB 369 CTGCTGAGTGTACACTGCGCTGCGGAGAGGAGCTGCGCTGAGTGTCTTTGGC 428
QY 108 LysPheLeuGlyLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeu 127
DB 429 TCTGCCCTCTGCAAGTGGGAGGAGGCTGCTTCAACATCAACTTCTAGCAGAGAGCCCTC 488
QY 128 IleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsnSerGln 147
DB 489 CTGCTGCGCTGATCATGACTTTTACCGCTACCTGAAACATAGTTCATGACCCAGCTGAC 548

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QY	148	ArprrkrrgylsleuleuAlaGluLysAlaValTyrValGlyValTrpPleProAlaLeu	167
Db	549	CGCGGGGGGGCCCCGGCCCCGGCTGACCCCTTACCTGCGCTGTGGGGCTCTGCGCTG	608
QY	168	LeuLeuthrThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSerGlnGly	187
Db	609	CTTTGCGCCCTGCCAGACTTCATCTTCTCTGCG-----GCCACAC	650
QY	188	AspAspArgTyr-----IleCysAspArgLeuTyrProAspSerLeuTrpMetVal	204
Db	651	GAACAGGCGCCCAACAGCCACCCACTGGCCAAATACAACTTCCCA---CAGGTGGCGGCACG	707
QY	205	ValPheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlnIleValIleLeuSer	224
Db	708	GCTCTGGGGGTGCTGCACGTGGTGGCTGGCTTTTGTGCGCCCTGCTGGTATGAGCCCTAC	767
QY	225	CysTrpCysIleIleIleIleSerLysLeuSerHisSerLysGlnHisGlnLysArgLysAla	244
Db	768	TGCTATGCGCCACATCTCCGCGCTGCTGTGGTTTCCAGGGCCACAGCGCGCTGCGGGCC	827
QY	245	LeuLysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrVal	264
Db	828	ATGCGGCTGCGTGTGGTGTGGTGTGGTGGCTTTGCCCTGCTGAGACCCCTATACACTG	887
QY	265	GlyIleSerIleAspSerPheIleLeuLeuGlnGlyValIleLysGlnGlyCysAspPheLeu	284
Db	888	GTTGTTGTTGGTGGACATCTTCATGACCTGGGGCTTTGGCCGCCACATCTGGCGGAA	947
QY	285	SerIleValHisLysTrpPleSerIleThrGlnAlaLeuAlaPhePheHisCysCysLeu	304
Db	948	AGCAGGGTACACGTGGGCCAATCGGTACCTCAGGCCCTGGGCTTACATCGTGTGCTTC	1007
QY	305	AsnProIleLeuTyrAlaPheLeuGlnAlaLysPheLysSerSerAlaGlnHisAlaLeu	324
Db	1008	AAACCCGCTGCTATGCTTGTGTAGGGGTCAAGTTCCGGAGCGGATGTGATGCTGCTC	1067
QY	325	AsnSerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgGlyLysHis	344
Db	1068	-----TTGGCGCTGGGGCTGCCCAACACAGAGAGGCTCCAG	1103
QY	345	SerSerValSerThrGlnJuserGlnSerSerSerPhe	356
Db	1104	AGCAGCCATCGTCTTCCCGCGGGATTCACTCCTGG	1139
RESULT 11			
US-09-880-107-3833			
Sequence 3833, Application US/09880107			
Patent No. US20020142981A1			
GENERAL INFORMATION:			
APPLICANT: Horne, Darci T.			
APPLICANT: Vockley, Joseph G.			
APPLICANT: Scheerf, Uwe			
APPLICANT: Gene Logic, Inc.			
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer			
FILE REFERENCE: 44921-5028-WO			
CURRENT FILING DATE: US/09/880,107			
PRIOR FILING DATE: 2001-06-14			
PRIOR APPLICATION NUMBER: US 60/7211,379			
PRIOR FILING DATE: 2000-06-14			
PRIOR APPLICATION NUMBER: US 60/237,054			
NUMBER OF SEQ ID NOS: 3950			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 3833			
LENGTH: 1670			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
OTHER INFORMATION: Genbank Accession No. US20020142981A1 X95876			
US-09-880-107-3833			
Alignment Scores:	8.82e-57	Length:	1670
Pred. No.:			

Score:	584.00	Matches:	124
Percent Similarity:	54.26%	Conservative:	67
Best Local Similarity:	35.23%	Mismatches:	139
Query Match:	31.28%	Indels:	22
DB:	10	Gaps:	5
US-09-367-052-2 (1-359) x US-09-880-107-3833 (1-1670)			
QY	12 AspaenrYrSerGIuGlIuValGIySerGIAspPYrAspSerAsn-----Lys	27	
DB	129 GAGAACTTCAGCTCTTCTATGACTATGAGAAAGAGAGAGTACGTGCTGACCTCC	188	
QY	28 GIuProCYsPheAlaGAspGIuAsnValHisPheAsnAlqIIlePheLeuProThrIIeYr	47	
DB	189 CCGCCCTCCACAGAGACTTCAGCCTTGAACTTCGACGGGGCTTCACAGCCCTTAC	248	
QY	48 PheIIleIlePheLeuThrGIYIleValGIyAsnGIyLeuValIIleLeuValMetGIyYr	67	
DB	249 AGCCCTCCTTCTCTCTGCTGGGCTGCTGGGCAAGCGCGGCTGACGCGCTGCTGAC	308	
QY	68 GIuIYsLysLeuArgSerMetThrAspLysTrAlqLeuHisLeuSerValAlaAspLeu	87	
DB	309 CGGCGAGACAGCCCTGACAGCAGCAGACACCTTCCTGCTACACCTGATGACAGACAG	368	
QY	88 LeuPheValIIeThrLeuProPheThrAlaValaAspAlaMetAlaAspTrIYrPheqly	107	
DB	369 CTGCTGGGTGACACTCTCCCTCTGGGCAAGTGAGCGCTGCCCTCACGTGGGTGGC	428	
QY	108 LysPheLeuCYsLysAlaValHisIleIleYrThrValAspLeuLeuYrSerSerValIleu	127	
DB	429 TCTGGCCTCTGCAAGGTGACAGCTCCCTCTTCAACATCACTTCTAGCAGAGCCCTC	488	
QY	128 IIleLeuAlaPheIIeSerLeuAspTrIYrLeuAlaIIleValHisAlaThrAsnSerGIu	147	
DB	489 CTGCTGGCGCTGATCAGCTTGACCGGTACCGTACGAACTTCAATGACCAAGCAGCTTAC	548	
QY	148 ArgProAlqYsLeuLeuAlaGIuLysAlaValIYrValGIyValTrIleProAlaLeu	167	
DB	549 CGCCGGGGGGCCCGCCCGCTGACCCCTCACCTGCTGGCTGTGGGGGCTGCTGCTG	608	
QY	168 LeuLeuThrIIeProAspPheIIePheIIaAspValSerGIuYAspIIeSerGIuqly	187	
DB	609 CTTTTCGCCCTCCAGACTTCACTTCTCTGTCG-----GCCACACAC	650	
QY	188 AspAspArgTYr-----IIeCYsAspArgLeuTYrProAspSerLeuTrpMeIYal	204	
DB	651 GACGAGCGCCTCAAGCCACCCACCTGACCAATGACACTTCCCA---CAAGTGGCGCCGACG	707	
QY	205 ValPheGIuPheGIuHisIleMeIYalGIyLeuIIleLeuProGIYIleValIIleuSer	224	
DB	708 GCTCGCGGGCTCCACCTGCTGGCTGCTTCTTGGCCCTGCTGGTCAATGGCCCTAC	767	
QY	225 CysTrYrCYsIIleIIeIleSerLysLeuSerHisSerLysGIuYHisGIuLysArgLysAla	244	
DB	768 TGCATAGCCACATCTGCGCTGCTGCTGTTCACAGGGGCGACGGCGCTGGGGCC	827	
QY	245 LeuLysTrnThrValIIleLeuIIleLeuAlaPhePheAlaCYsTrIleuProTrYrVal	264	
DB	828 ATGCGCGCTGGGTGGTGGCTGGTGGCTTGGCCCTGCTGGTGAACCCCATACCTG	887	
QY	265 GIYIleSerIIeAspSerPheIIeLeuLeuGIYalIIeLysGIuqlyCYsAspPheGIu	284	
DB	888 GNGGTGCTGGTGAATCTCATGACCACTGGCGCTTGGCCCGCACTGATGGCCGAGAA	947	
QY	285 SerIIleValHisLysTrIleSerIIeThrGIuAlaLeuAlaPhePheHisCysCysLeu	304	
DB	948 AGCAGGTAAGACGTGGCCAGTCCGCTCACTTACAGCGCTGATCATCAGCGCTGC	1007	
QY	305 AsnProIIleLeuTrYrAlaPheLeuIIleLysLysPheLysSerSerAlaGIuHisAlaLeu	324	
DB	1008 AACCCGCTGCTATAGCCTTGTAGGGGTCAAGTTCGGGAGACGATGTGATGCTGCTC	1066	
QY	325 AsnSerMetSerArgIYsSerSerLeuLysIIleLeuSerLysGIYLysArgGIYHis	344	

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Db      1068 -----TTGGCGCTGGGCTGCCCAACCAAGAGAGGCTCCAG 1103
      |||:::|
QY      345 SerSerValSerThrGluSerGluSerSerSerPhe 356
      ||:::|
Db      1104 AGGCAGCCATGCTCTTCCCGCCGCGATTCATCTCG 1139

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QY 12 AspaNtYrSerGluValGlySerGlyAspTyrAspSer-----AsnLys 27
Db 374 GAGAACTTCACTCTCTCTATGACTATGAGAGAAAAGAGATGAMTCTGCTATACCTCC 433
QY 28 GluProCysPheIleGaspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyr 47
Db 434 CCGGCTCTCCCAAGAGACTTCAAGCTGAACTTCGACGGGCTCTCCAGCCCTCWCAC 493
QY 48 PheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMetGlyTyr 67
Db 494 AGCTCTCTCTTCTGCTGGGCTGCTGGCAACGGCGGTGGCAAGCCGCTCTGTCAGC 553
QY 68 GluLysLysLeuArgSerMetThrAspLysTyrArgHisLeuSerValAlaAspLeu 87
Db 554 CGGGGAGACGCCGAGAGACGACGACCTTCCTCGCTCCACCTAGCTGACAGACACR 613
QY 88 LeuPheValIleThrLeuProPheThrAlaValAlaMetAlaAspTyrTyrPheGly 107
Db 614 CTGCTGTGTGCTGACACTGCTGCTGAGCTGAGCGCTGCGCTGACGAGGCTCTTGC 673
QY 108 LysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerValLeu 127
Db 674 TCTGACCTCTCAAGTGGCAGGTGCTCTTCAACATCACTTCTACGAGGACCTCTC 733
QY 128 IleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsnSerGln 147
Db 734 CTGCTGGCTGCTATCAGCTTGTGACCGCTACCTGAAACATAGTTCACTGACCCAGCTTAC 793
QY 148 ArgProArgLysLeuLeuAlaGlyLysAlaValTyrValGlyValTyrIleProAlaLeu 167
Db 794 CGCGGGGGGCGCGCGCGCGGTGACCTCTGACCTGCTGCTGCTGCTGCTGCTGCTG 853
QY 168 LeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSerGlnGly 187
Db 854 CTTTTCGCGCTCCCAAGACTTATCTCTGTCG-----GCCACACAC 895
QY 188 AspaAspArgTyr-----IleCysAspArgLeuTyrProAspSerLeuTyrMetVal 204
Db 896 GACGAGCGCTCAAGCCACCCACCATCAATCAACTGCCA---CAGGTGGGCGCGCACG 952
QY 205 ValPheGlnPheGlnHisIleMetValGlyLeuLeuProGlyIleValIleLeuSer 224
Db 953 GCTGTGCGGTGCTGCAAGCTGCTGCTGCTTTCGCTGCTGCTGCTGCTGCTGCTGCT 1012
QY 225 CysTyrCysIleIleIleSerLysLeuSerHisSerLysGlnHisGlnLysArgLysAla 244
Db 1013 TGTATGCCCCACATCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1072
QY 245 LeuLysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrLeuProTyrTyrVal 264
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QY 265 GlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGlu 284
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QY 305 AsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeu 324
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QY 325 AsnSerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHis 344
Db 1313 -----TTGGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1348
QY 345 SerSerValSerThrGluSerGluSerSerPhe 356
Db 1349 AGGAGCCATGCTCTTCCCGCGGAGATTCACTGCTGG 1384

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RESULT 14
US-10-120-394-19
; Sequence 19, Application US/10120394
; Patent No. US20020160015A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Timothy N.C.
; Power, Christine A.
; TITLE OF INVENTION: CHEMOKINE RECEPTOR ABLE TO BIND TO MCP-1, MIP-1 ALPHA AND/OR RANTES AND ITS USES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESS: NIXON & VANDERHAYE P.C.
; STREET: 1100 NO. US20020160015A1th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 09/614,256
; FILING DATE: 12-JUL-2000
; APPLICATION NUMBER: US 08/875,573
; FILING DATE: 31-OCT-1997
; APPLICATION NUMBER: PCT/GB96/00143
; FILING DATE: 24-JAN-1996
; APPLICATION NUMBER: GB 9501683.8
; FILING DATE: 27-JAN-1995
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 183..1262
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-120-394-19

Alignment Scores:
Score: 2,93e-55 Length: 1607
Pred. No.: 570.50 Matches: 120
Percent Similarity: 57.01% Conservative: 63
Best Local Similarity: 37.38% Mismatches: 125
Query Match: 30.56% Indels: 13
DB: 9 Gaps: 6

US-09-367-052-2 (1-359) x US-10-120-394-19 (1-1607)
QY 1 MetGluProIleSerValSerIleTyrThrSerAspaNtYrSerGluValGlySer 20
Db 183 ATGAACCCACAGGATATGACAGATACCACTCTGCAT-----GAAAGCATATACAGC 233
QY 21 GlyAsp-----TyrAspSerAsnLysGluProCysPheArgAspGluAsnValHisPhe 38
Db 234 AATTACTATCTGTATGAAGATATCCCAAGCTTGCACCAAGAAGAGCATCAAGCATTTT 293
QY 39 AsnArgIlePheLeuProThrIleTyrPheIleIlePheLeuThrGlyIleValGlyAsn 58
Db 294 GGGAGAGCTCTTCGCGCCCACTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 353
QY 59 GlyLeuValIleLeuValMetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyr 78
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Qy 99 AspaIaMetAlaAspTyrPheGlyLysPheLeuCysLysAlaValHisIleTyr 118
Db 474 TATCAGACAGACCGAGTGGTGGCTGAGCTGTCAGAGATGATTCCTGATGATAC 533
Qy 119 ThrValAsnLeuTyrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeu 138
Db 534 TTGCTGGGCTTTACAGGCGATATCTTTGCTCATGCTCATGACATGATGATACCTG 593
Qy 139 AlaIleValHisAlaThrAsnSerGlnArgProArgLysLeuAlaGluLysAlaVal 158
Db 594 GCGATAGTGCACGCGGGTGTTCCTTGAGGGCAGAGACCTGATTTAGGGTCATCACC 653
Qy 159 TyrValGlyValTrrPheIleAlaLeuLeuLeuThrIleProAspPheIlePheAlaAsp 178
Db 654 AGTTGGCTACATGTCAGTGGCTGTGTGCGCTCCCTCTGCTTCTGCTGAGCAGCT 713
Qy 179 ValSerGlnGlyAspIleSerGlnGlyAspAspArgTyrIleCysAspArgLeuTyrPro 198
Db 714 TGT-----TATACTGAGCGCAGACCATACCTAC--TGCAGAAACCAAGTACTCT 758
Qy 199 -----AspSerLeuTrrPheValValPheGlnPheGlnHisIleMetValGlyLeuIle 216
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Qy 217 LeuProGlyIleValIleLeuSerCysTyrCysIleIleIleSerLysLeuSerHisSer 236
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Qy 257 AlaCysTrrPheProTyrTyrValGlyIleSerIleAspSerPheIleLeuLeuGlyVal 276
Db 939 GGGTCTGACACCTTACACATAGTCTCTTCCAGAGACCTGCTGAGCTGAGCTGAGCTG 998
Qy 277 IleLysGlnGlyCysAspPheGluSerIleValHisLysTrrPheIleSerIleThrGluAla 296
Db 999 CTT---CAGGACTGCACCTTGAAGATACCTGGACTATGCCATCCAGCGCACAGAAACT 1055
Qy 297 LeuAlaPhePheHisCysCysLeuAsnProIleLeuTyrAlaPheLeuGlyAlaLysPhe 316
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317 Lys 317
1116 CGC 1118

RESULT 15
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: Sequence 19, Application US/09764413
: Publication No. US20020187930A1
: GENERAL INFORMATION:
: APPLICANT: Wells, Timothy N.C.
: TITLE OF INVENTION: A CHEMOKINE RECEPTOR ABLE TO BIND TO
: POWER, CHRISTINE A.
: MCP-1, MIP-1 ALPHA AND/OR RANTES. ITS USES
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NIXON & VANDERHIVE P.C.
: STREET: 1100 NO. US20020187930A1th Giebe Rd. 8th floor
: CITY: Arlington
: STATE: VA
: COUNTRY: USA
: ZIP: 22201-4741
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,413
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/875,573
FILING DATE: <Unknown>
APPLICATION NUMBER: GB 9501683.8
FILING DATE: 27-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-172
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1607 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 183..1262
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-764-413-19
Alignment Scores:
Pred. NO.: 2,93e-55 Length: 1607
Score: 570.50 Matches: 120
Percent Similarity: 57.01% Conservative: 63
Best Local Similarity: 37.38% Mismatches: 125
Query Match: 30.56% Indels: 13
DB: Caps: 6
US-09-367-052-2 (1-359) x US-09-764-413-19 (1-1607)

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Qy 1 MetLupProIleSerValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySer 20
Db 183 ATGAGACCCAGCAGATATGAGATACGATACGACCTCGAT-----GAAAGCATATACAGC 233
Qy 21 GlyAsp-----TyrAspSerAsnLysGluProCysPheArgAspGluAsnValHisPhe 38
Db 234 AATTACTATCTGTATGAAAGATATCCCAAGCTTGCACCAAGAGATCAAGGATTT 293
Qy 39 AsnArgIlePheLeuProThrIleTyrPheIleIlePheLeuThrGlyIleValGlyAsn 58
Db 294 GGGAGCTCTTCTGCCCCCAGCTGATATCTTGGTTTGTATTTGGCTGCTGGAAT 353
Qy 59 GlyLeuValIleLeuValMetGlyTyrGlnLysLysLeuArgSerMetHisAspLysTyr 78
Db 354 TCTGTGGTGGTTCGTCGCTGTCCTCAATATACAGCGGCTGACGCTCAATGATGATGTAC 413
Qy 79 ArgLeuHisLeuSerValAlaAspLeuPheValIleThrLeuProPheIleVal 98
Db 414 CTGCTCAACCTTGGCAGCTGCGATCTGCTCTGCTTTTCCCTTTTGGGGCTAC 473
Qy 99 AspaIaMetAlaAspTyrPheGlyLysPheLeuCysLysAlaValHisIleTyr 118
Db 474 TATCAGACAGACCGAGTGGTGGCTGAGCTGTCAGAGATGATTCCTGATGATAC 533
Qy 119 ThrValAsnLeuTyrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeu 138
Db 534 TTGCTGGGCTTTACAGGCGATATCTTTGCTCATGCTCATGACATGATGATACCTG 593
Qy 139 AlaIleValHisAlaThrAsnSerGlnArgProArgLysLeuAlaGluLysAlaVal 158
Db 594 GCGATAGTGCACGCGGGTGTTCCTTGAGGGCAGAGACCTGATTTAGGGTCATCACC 653

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 16:49:14 ; Search time 1186 Seconds

(without alignments)
4902.344 Million cell updates/sec

Title: US-09-367-052-2

Perfect score: 1867
Sequence: 1 MEPISTVSTYSDNYSEEVS.....KRGHSVSTSESSSFHSS 359

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Sequences: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Command line parameters:
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-Q=con2.1/USPTO.spool/US09367052/runat_10072003.100045.10395/app.query.fasta.1.519
-DB=EST -QFMT=fastap -SUFFIX=1st -MINMATCH=0.1 -DOOPCL=0 -DOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR.SCORE=DCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09367052.ecgn.1.1.1456 -runat_10072003.100045.10395 -NCPU=6 -ICPU=3
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-FEAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: em_esthum:*
3: em_estlin:*
4: em_estlm:*
5: em_estlov:*
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8: em_hic:*
9: gb_estcl:*
10: gb_estcl2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estlm:*
16: em_estlm:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_mam:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1422.5	76.2	1051	13	BM545259
2	1238.5	66.3	910	13	BM762229
3	1196	64.1	950	14	BM718617
4	1188	63.6	891	13	BM182463
5	1179	63.1	1034	14	BM920800
6	1172	60.1	827	13	BM761664
7	1098	58.8	913	13	BM051973
8	1096.5	58.7	875	13	BM756157
9	1093.5	58.6	905	13	BM1754094
10	1086.5	58.2	765	13	BM387369
11	1082.5	58.0	750	12	BM613352
12	1027.5	55.0	746	13	BM917014
13	987.5	52.9	782	12	BM685801
14	986	52.8	846	12	BM338608
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16	979	52.4	958	12	BM174412
17	975.5	52.2	702	13	BM1761118
18	974.5	52.2	582	12	BM145042
19	973.5	52.1	680	14	BM109515
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21	967.5	51.8	728	9	AU117058
22	958	51.3	955	12	BM173867
23	942	50.5	753	13	BM915636
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25	924.5	49.5	703	13	BM1765768
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29	907.5	48.6	793	9	AA182270
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34	881	47.2	585	10	BM627479
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ALIGNMENTS

RESULT 1	BM545259	1051 bp	mrna	linear	EST 20-FEB-2002
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DEFINITION	AGENCOURT 6497171 NIH_MGC_124 Homo sapiens CDNA clone IMAGE:5726963				
ACCESSION	BM545259				
VERSION	BM545259.1				
KEYWORDS	5', mRNA sequence.				
SOURCE	EST.				
ORGANISM	human.				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 1051)				
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.jnl.gov>
Plate: LLM12/720 row: e column: 12
High quality sequence start: 20
High quality sequence stop: 753.
Location/Qualifiers

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cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

BASE COUNT 240 a 302 c 238 g 271 t
ORIGIN

Alignment Scores:

Pred. No.: 5,226-165 Length: 1051
Score: 1422.50 Matches: 281
Percent Similarity: 91.598 Conservative: 24
Best Local Similarity: 84.388 Mismatches: 18
Query Match: 76.198 Indels: 10
Gaps: 1

US-09-367-052-2 (1-359) x BM545259 (1-1051)

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QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
DB 197 ATCTACTCCATCATCTTTCTTAACGTGCGCATGTGGSCAATGATGTGATCTGTGTCATG 256
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DB 437 GTCTCATCTCTGCGCTCATGCTGACGCGCTACCTGCGCATGTCACAGCCACCAAC 496
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTyrIlePro 165
DB 497 AGTCAGAGGCCCAAGAACCTGTGGCTGAAAAGGTGCTATGTGGCGCTGGATCCCT 556

QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
DB 557 GCCCTCCGCTGACATATCCCGACTTCTCTTTGGCAACGTC-----AGT 601
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DB 602 GAGGACATGACAGATATATCTGTACCGCTTACCCCAATGACTGTGGTGGTCTG 661
QY 206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSerCys 225
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QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrLeuProTyrTyrValGly 265
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QY 324 uAsnSerMet-SerArgGlySerSerLeu 333
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RESULT 2
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DEFINITION B1762229 910 bp mRNA linear EST 25-SEP-2001
603049139F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189552 5',
mRNA sequence.
ACCESSION B1762229
VERSION B1762229.1 GI:15753807
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 910)
NIH-MGC <http://mgc.nci.nih.gov/>.
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.jnl.gov>
Plate: LLM14/73 row: m column: 09
High quality sequence stop: 827.
Location/Qualifiers

FEATURES
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/clone="IMAGE:5189552"
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/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA

source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH-MGC Library."

BASE COUNT 210 a 260 c 208 g 232 t
ORIGIN

Alignment Scores:

Pred. No.: 2,59e-142 Length: 910
Score: 1238.50 Matches: 240
Percent Similarity: 92.20% Conservative: 20
Best Local Similarity: 85.11% Mismatches: 15
Query Match: 66.34% Indels: 7
DB: 13 Gaps: 1

9-367-052-2 (1-359) x B1762229 (1-910)

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QY 6 ValSerIleTyrThSerAspAsnTyrSerGluValAlGlySerGlyAspTyrAspSer 25
DB 83 ATCACTATATACACTTCACTGATTAACACCCGAGAAATGGCGCTCAGGGGACTATGACTCC 142
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
DB 143 ATGAGAGAACCTGTTTCGGTGAAGAAATGCTATTCATAATTAATCTCTGCGCCACC 202
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValAlGlyAsnGlyLeuValIleLeuValMet 65
DB 203 ATCTACTCATCATCTTCTTACTGTCGATTTGGGCAATGATGATGCTACTCTGCTCATG 262
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
DB 263 GGTTCACGAGAACTGAGAGCATGAGCGAGCATGAGCGCTGCTCAGCTGCTGCGCC 322
QY 86 AspLeuLeuPheValIleThrLeuProPheThrPalaValAlaMetAlaAspTyrPyr 105
DB 323 GACCTCTCTTGTATACAGCTTCTGCGAGGTGATGATGCGGCAAGCTGGTAC 382
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThValAsnLeuTyrSerSer 125
DB 383 TTGGGAACTTCTTATGACAGGCACTGATCATCTACACAGTCACTCCTACAGCACT 442
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
DB 443 GTCCCTATCTTGCGCTTCACTGAGTGGACCGCTGCTGCGCATGCTCCACGCCACAAAC 502
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
DB 503 AGCTGAGAGGCCAAGAGAGCTGTGGCTGAAGAGGTGCTATGTGGCTGTGATCCCT 562
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
DB 563 GCCCTCTGCTGACTATTCGCCGACTTCATCTTGGCAAGCTC-----AGT 607
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
DB 608 GAGGAGAGATGACAGATATATCTGTGACCGCTTCTCCCAAGACTTGTGGGTGGTGG 667
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerGly 225
DB 668 TACCGATTTCACACATCATGTTGGCTTATCTGCGCTGGGATTTGTCTCTGCTGCTGC 727
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
DB 728 TATTCATATATCATCTCCAAAGCTGCACACCTCAAGGGGCAAGAGCGCAGCGCCCTC 787
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAla-CysTrpLeuProTyrTyrValGln 265
DB 788 CAGACCACAGTATCTCTGCTTCTTCTGCGCTGCTGCTGCTTACTACTTTGG 847

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QY 265 YlleSerIleAsp-SerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGln 285
DB 848 GATCAGCATCATCTTCTTCTTCTGGAATCATCATCAAGGAGGTGTACATTTGANA 907
QY 285 er 285
DB 908 AC 909

RESULT 3
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LOCUS B0718617
DEFINITION AGENCOURT 8304537 lupskl.sympathetic_trunk Homo sapiens CDNA clone
IMAGE:6193609 5', mRNA sequence.
ACCESSION B0718617
VERSION B0718617.1 GI:21857514
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 950)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strussberg, Ph.D.
Email: cgep@remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL13597 row: 1 column: 02
High quality sequence stop: 659.

FEATURES

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/db_xref="taxon:9606"
/clone="IMAGE:6193609"
/clone_1ib="lupskl_sympathetic_trunk"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/note="Vector: PCMV-SPORT6 (Life Technologies); Site_1: NotI, Site_2: SalI; CDNA made by oligo-dT priming. Directionally cloned using the following adaptors:
5'-GACTAGTTCTAGATGCGGAGCGGCGGCTT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

BASE COUNT 223 a 270 c 217 g 238 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 5.11e-137 Length: 950
Score: 1196.00 Matches: 241
Percent Similarity: 88.51% Conservative: 21
Best Local Similarity: 81.42% Mismatches: 25
Query Match: 64.06% Indels: 9
DB: 14 Gaps: 2

US-09-367-052-2 (1-359) x B0718617 (1-950)

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QY 6 ValSerIleTyrThSerAspAsnTyrSerGluValAlGlySerGlyAspTyrAspSer 25
DB 83 ATCACTATATACACTTCACTGATTAACACCCGAGAAATGGCGCTCAGGGGACTATGACTCC 142

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QY 26 Asnysgluprocyspheargaspcluasvalhisphasnargliepheleuprothr 45
 DB 143 ATGAAGAAACCCGTTTCCTGGAAGAAATGCTATTTCAATAAATCTCTGCCACC 202
 QY 46 Iletryrphellellepheleuthrcllyllevalglyasnglyleuvalilleuvalmet 65
 DB 203 ATCTACTCCATCATCTTCTTAACGTGGCATTTGGGCAATGATGGTATCTCTGCTATG 262
 QY 66 GlytryglnlylslysleuargsermethrapslytryargleuhsleuSERvalala 85
 DB 263 GGTTCAGAGAAAGAACTGAGAAAGCATGACGCAAGTACAGAGCTGACCTGCTACGTGCC 322
 QY 86 AspleuLeuphevalillethrleuprophetrralavalaaspalametalaasprtryr 105
 DB 323 GACCTCCTCTTGTTCATCAGCTTCCCTTGGGAGTTGATGCCGTGCAAACTGCTAC 382
 QY 106 PheglylyspheluCysLysAlaValHisIlelletryrthvalasnleuTyrSer 125
 DB 383 TTTGGGAACCTTCATGCAAGGCACTGCTCATCTACACAGTCAACCTCTACAGCAGT 442
 QY 126 ValIleuIleleuAlaPheIleSerleuAspartryrleuAlaIleValHisAlathrasn 145
 DB 443 GTCCCATCTGGCTTATCATGCTGACCGCTACCTGGCCATGCTCCAGCCACGAC 502
 QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrrIlePro 165
 DB 503 AGTCAGAGGCCAAGAGAGCTGTGGCTGAAAAGTGCTATGTTGGGCTGCTGATCCCT 562
 QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheIleAlaAspValSerGlnGlyAspIleSer 185
 DB 563 GCCCTCCTGCTGACTATTCGCCAGACTTCATCTTGGCAACGTC-----AGT 607
 QY 186 GlnGlyAspAspartryrIleCysAspartryrLeuTyrProAspSerLeuTrrPheValVal 205
 DB 608 GAGCAGATGACAGATATATCTGTACCGCTTCTACCCCAATGACTGTGAGTGTGTG 667
 QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
 DB 668 TTCAGATTTCAGACATCATGTGGTCTTATCTCGCTGATGATGTCATCTGCTGCTGC 727
 QY 226 TyrCysIlellelleSerLysLeuSerHisSerLysGlnGlnLysArgLysAlaLeu 245
 DB 728 TATTCATATATCATCTCAAGCTGTCACACTCCAGGCCACCAAGCCGCAAACTCCCT 787
 QY 246 LysThrTrpValIleLeuIleLeuAla-PhePheAlaCysTrpLeuProTyrTyr-ValG 265
 DB 788 CAGAACACAGNATCTCATCTGCTTCTTCTGCGCTGGTGGCTTACTACTACATG 847
 QY 265 LysIleSerIleAspSer-PheIleLeuLeuGlyValIleLys--GlnGlyCysAspPhe 283
 DB 848 GGATCAGCATGAAATCCCTTCATCTCTCGATCCCTCAAGACCAAGGGGGGAATTTT 907
 QY 284 GluSerIleValHisLysTrpIleSerIleThrGluAlaLeu 297
 DB 908 AAAAATTTGTCACAGAGATTTCCCATCCCGAAGGCTT 949
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 DEFINITION 603033815f1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174978 5',
 mRNA sequence.
 ACCESSION B1824663
 VERSION B1824663.1 GI:15936213
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 891)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>,
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMU at:
<http://image.llnl.gov>
 Plate: LMU1435 row: n column: 03
 High quality sequence stop: 827.
 Location/Qualifiers
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 /clone="IMAGE:5174978"
 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector:
 pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH-MGC Library."
 BASE COUNT 207 a 250 c 205 g 229 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 4,52e-136 Length: 891
 Score: 1188.00 Matches: 236
 Percent Similarity: 89.68% Conserves: 16
 Best Local Similarity: 83.99% Mismatches: 21
 Query Match: 63.63% Indels: 8
 DB: 13 Gaps: 2
 US-09-367-052-2 (1-359) x B1824663 (1-891)
 QY 6 ValSerIletryrthnseraspasntyrserclugluvaliglyserglyasptryrpsr 25
 DB 64 ATCAGTATATACCTTCGATGATACACCGAGAAATAGGCTCAGGGACTATGACTCC 123
 QY 26 Asnysgluprocyspheargaspcluasvalhisphasnargliepheleuprothr 45
 DB 124 ATGAAGAAACCCGTTTCCTGGAAGAAATGCTATTTCAATAAATCTCTGCCACC 183
 QY 46 Iletryrphellellepheleuthrcllyllevalglyasnglyleuvalilleuvalmet 65
 DB 184 ATCTACTCCATCATCTTCTTAACGTGGCATTTGGGCAATGATGGTATCTCTGCTATG 243
 QY 66 GlytryglnlylslysleuargsermethrapslytryargleuhsleuSERvalala 85
 DB 244 GGTTCAGAGAAAGAACTGAGAAAGCATGACGCAAGTACAGAGCTGACCTGCTACGTGCC 303
 QY 86 AspleuLeuphevalillethrleuprophetrralavalaaspalametalaasprtryr 105
 DB 304 GACCTCCTCTTGTTCATCAGCTTCCCTTGGGAGTTGATGCCGTGCAAACTGCTAC 363
 QY 106 PheglylyspheluCysLysAlaValHisIlelletryrthvalasnleuTyrSer 125
 DB 364 TTTGGGAACCTTCATGCAAGGCACTGCTCATCTACACAGTCAACCTCTACAGCAGT 423
 QY 126 ValIleuIleleuAlaPheIleSerleuAspartryrleuAlaIleValHisAlathrasn 145
 DB 424 GTCCCATCTGGCTTATCATGCTGACCGCTACCTGGCCATGCTCCAGCCACGAC 483
 QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrrIlePro 165
 DB 484 AGTCAGAGGCCAAGAGAGCTGTGGCTGAAAAGTGCTATGTTGGGCTGCTGATCCCT 543
 QY 166 AlaLeuLeuLeuThrIleProAspPheIlePhe-AlaAspValSerGlnGlyAspIleSe 185

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 544 GCCCTCCTGCTGACTATTCGCCGACTTCATCTTGCCCAAGTC-----AG 588
 185 rGInGlyAspAspArgTrIleCysAspArgLeuTyrProAspSerIleuTrpMetVal 205
 589 TGAAGCAGATGACGATATATCTGTGTGACCCCTCTTACCACCAATACTGTGGGTGTGT 648
 205 lPheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
 649 GTTCACATTTTCAGACATCATGTTGGCCTTATTCCTCCCTGATTTGTCATCCTGTCCTG 708
 225 sTyrCysIleIleIleSerIleuSerHisSerLysGlyHisGlnLysArg-LysAlaL 245
 709 CTATTGCATTATCATCTCCCAAGCTGCACACTCCAGGCCACAGCAAGGCCAAGGCC 768
 245 eulysTrh-----ThValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrIle 264
 769 TCAAGACACACACTCATCCCTCATCTGCTTCTTCTTCTGCTGTGGCTGCTTACTACT 828
 264 alGlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPhe 283
 829 TGGGAATCAGATCAATCTCTCCCTCCTCTCGAATATCATCAAGCAAGGTGTAAGTTT 887

RESULT 5
 BM920800 1034 bp mRNA linear EST 12-MAR-2002
 LOCUS AGENCOURT 6706081 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5752047
 DEFINITION 5', mRNA sequence.
 ACCESSION BM920800
 VERSION BM920800.1 GI:19371179
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE
 1 (bases 1 to 1034)
 NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: LHAM12785 row: j column: 16
 High quality sequence stop: 667.
 Location/Qualifiers

FEATURES

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 /db_xref="taxon:9606"
 /clone="IMAGE:5752047"
 /clone_1id="NIH_MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis. Vector:
 pCW-SPORE6; Site_1: NOTI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC library."
 BASE COUNT 231 a 302 c 236 g 265 t
 ORIGIN

Alignment Scores: 7.47e-135 Length: 1034
 Score: 1179.00 Matches: 243

Percent Similarity: 90.56% Conservative: 16
 Best Local Similarity: 84.97% Mismatches: 11
 Query Match: 63.15% Indels: 16
 DB: 14 Gaps: 3

US-09-367-052-2 (1-359) x BM920800 (1-1034)

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 86 ATCAGTATATACACTTTCAGATTAACACTACCGAGAAATGGGCTCAGGGACTATGACTCC 145
 26 AsnLysGlnProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
 146 ATGAAGAACCCCTGTTCCCGAAGAAATGCTAATTTCAATAAATCTTCCTCCACCC 205
 46 IleTyrPheIleIlePheLeuThrGlyTlleValGlyAsnGlyLeuValIleLeuValMet 65
 206 ATCTACTCCATCATCTTCTTAACGCGATGTGGCAATGGATGGTCACTCCGTCATG 265
 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
 266 GGTATACCAAGAAACTGACAGCATGACGACAGTACAGCTGCACCTGTCCAGTGGCC 325
 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
 326 GACCTCCTCTTTGTATCATCAGCCTTCCCTTGGCGAGTGTGCGGCAAACTGGTAC 385
 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrTrhValAsnLeuTyrSerSer 125
 386 TTTGGGAATCTTCCTATCATCAAGGACGATCATCTATCAACAGTCAACCTCTTACAGCAGT 445
 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
 446 GTCTCTCATCTCGGCTTCATCATCTGACCCGCTTACCTGGCCATCTCCACGCCACCAAC 505
 146 SerGlnArgProArgLysLeuLeuAlaGlyLysAlaValTyrValGlyValTyrIlePro 165
 506 AGTCAGAGGCCAAGAGAGCTGTGGTGAAGAGTGCTATGTTGGCGTCTGATCCCT 565
 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
 566 GCCCTCTGCTGACTATTTCCCGACTTCATCTTCCCAAGTC-----AGT 610
 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
 611 GAGCAGATGACAGATATATCTGTGACCGCTTACCCCAATGACTTGTGGTGTGTG 670
 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
 671 TTCAGTTTCAGCACATCATGTTGGCCTTATCTGCTGATTTGTCATCTGCTCTGC 730
 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHis-GlnLysArgLysAla-L 245
 731 TATTGCAATTATCATCTCCAACTGTCACTCCAAAGGCCACCCAGAGGCCAAGGCC 790
 245 eulysTrhTrhValIleLeuIleLeuAlaPhe-----PheAlaCysTrpLeuProT 262
 791 TCAAGACACACAGTATCTCTCTGCGCTTCTTCCCTGTGGTGTGCTC-----CTTA 844
 262 TyrTyrVal-GlyIleSerIleAspSer-PheIleLeuLeuGly-ValIleLys-GlnGly 280
 845 ACTACATTTGGGATCAGATGATGATCTCTTTCATCTCTCTGGAATCATCAAGCCAAAGGT 904
 281 CysAsp 282
 905 TGTGAG 910

RESULT 6
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 DEFINITION 603046395F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186878 5',
 mRNA sequence.
 ACCESSION B1761664

VERSION B1761664.1 GI:15753242
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo; 1 (bases 1 to 827)
 REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Plate: LLM11466 row: m column: 23
 High quality sequence stop: 827.
 Location/Qualifiers
 1. 827
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector: PCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous, pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH-MGC library."
 BASE COUNT 190 a 232 c 194 g 210 t 1 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 6.04e-128 Length: 827
 Score: 1122.00 Matches: 224
 Percent Similarity: 93.33% Conservative: 14
 Best Local Similarity: 87.84% Mismatches: 11
 Query Match: 60.10% Gaps: 8
 Indels: 1
 Gaps: 13
 US-09-367-052-2 (1-359) x B1761664 (1-827)
 Oy 6 Valserlelyrrthrtseraspasntyrserclugluvalaiglysergiyasprryaspser 25
 Db 83 ATCAGTATATACCTTACATGATACACCGAGGAATGGCTCAGG-GACTATGACTCC 141
 Oy 26 Asnlysgluprocysphearqaspgluasnvahisphesanaqgilepheleuprothr 45
 Db 142 ATGAGGACACCTCTTCCGAGAGAAATCTTAATTCATAAATCTCTCCACACC 201
 Oy 46 lletyrpheelieilepheleuthrglyllevaiglyasnlglyleuvalilleuvalmet 65
 Db 202 ATCTACTCCATCATCTTCTTAACGTGCAATGTGGCAATGATGTGCATCTGCTCATG 261
 Oy 66 GlytyrGlnlyslsleuAargsermethrAsplystyrtatgdeuHlsleuSerVala 85
 Db 262 GGTATACAGAAAACAGAGAGCATGACGCAAGTACAGAGCTGCACCTGTCACTGCC 321
 Oy 86 AspleuLeuPheValillethLeuProPheThrPalavalaspaLametalAspTrpTyr 105
 Db 322 GACCTCTCTTTGTCATCAGCCTTCTCTGCGCAGTGTATGCCGTGGCAACTGTGATC 381
 Oy 106 PheGlylspPheLeuCySlasAlaValHisIleIleIleIleIleIleIleIleIleIle 125

Db 382 TTGGGAACCTTCATGCAAGCGATCCATGTCATATACACAGTCAACCTCTACAGACT 441
 Oy 126 ValIleuIleLeuAlaPheIleSerLeuAsparGlyLeuAlaIleValaHisAlaThrAsn 145
 Db 442 GTCCCTCATCTCGGCTTCATCAGCTGGACCGCTACCTGGCCATCTGCCACGCCACMAC 501
 Oy 146 SerGlnArgProArglyslsleuAlaGlyAlaValaValaIleValaIleValaIlePro 165
 Db 502 AGTCAGAGCCCAAGAAAGCTGTGGCTGAAAAGGTGGTGTATATGTNGCGCTGTGATCCCT 561
 Oy 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValaSerGlnGlyAspIleSer 185
 Db 562 GCCCTCTGCTGACTATTCGCCGACTTCATCTTGGCCAACTC-----AGT 606
 Oy 186 GlnGlyAspAsparGlyIleCysAsparGlyLeuTyrProAspSerLeuTyr-MetVala 205
 Db 607 GAGGCAATATACAGATATATCTGTGACCGCTTACCCCAATACCTGTGGTGGTGTCT 666
 Oy 205 lPheGlnPheGlnHisIleMetValaGlyLeuIleLeuProGlyIleValIleLeuSerCy 225
 Db 667 GTTCAGTTTCAGACATCATGTTGGCTTATCTCCCTGATATGTCTATCTCTGTC 726
 Oy 225 sTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAla 245
 Db 727 CTATTCATATATCATCTCAAGCTGTCACTCCAGGCCACAGGCCAGAGCCAGGC-CT 784
 Oy 245 ulysThrThrValIleIleLeuAlaPhePheAlaCysTrp 259
 Db 785 CAGAGCCACAGTCATCTCATCTCGGCTTCTTCCCTGTGG 827
 RESULT 7 913 bp mRNA linear EST 07-NOV-2001
 LOCUS BM051973 60363887F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:5419890 5',
 DEFINITION mRNA sequence.
 ACCESSION BM051973
 VERSION BM051973.1 GI:16781240
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo; 1 (bases 1 to 913)
 REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Plate: LLM1873 row: j column: 19
 High quality sequence stop: 723.
 Location/Qualifiers
 1. 913
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5419890"
 /clone_1lb="NIH_MGC_8"
 /lab_host="DH10B (phage-resistant)"
 /tissue_type="Burkitt lymphoma"
 /note="Organ: lymph. Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Site-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit

BASE COUNT 217 a 254 c 215 g 227 t
ORIGIN

Alignment Scores:

Pred. No.: 6.64e-125 Length: 913
Score: 1098.00 Matches: 233
Percent Similarity: 88.38% Conservative: 18
Best Local Similarity: 82.04% Mismatches: 19
Query Match: 58.81% Indels: 14
DB: 13 Gaps: 2

US-09-367-052-2 (1-359) x BM051973 (1-913)

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*QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
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Db 82 ATCACTATATACACTTTCAGATTAACACCGAGGAAATGGGCTCAGGGGACTATGACTCC 141
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
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QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
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QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
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    562 GCCCTCCCTGCTGACTATTCCGCACTTCATCTTGGCAACGTC-----AGT 606
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrMet-ValVal 205
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RESULT 8
B1756157
LOCUS

B1756157 875 bp mRNA linear EST 25-SEP-2001

DEFINITION 603030061F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5200238 5',
mRNA sequence.
ACCESSION B1756157
VERSION B1756157.1 GI:15747735
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 875)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Place: LNL11501 row: 3 column: 15
High quality sequence stop: 799.
Location/Qualifiers

FEATURES

source

1..875
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/clone="IMAGE:5200238"
/clone_11b="NIH_MGC_114"
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/note="Organ: brain; Vector: pCMV-Sport6; Site: 1: NotI;
Site: 2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
BASE COUNT 198 a 244 c 206 g 227 t
ORIGIN

Alignment Scores:

Pred. No.: 9.53e-125 Length: 875
Score: 1096.50 Matches: 229
Percent Similarity: 90.15% Conservative: 18
Best Local Similarity: 83.58% Mismatches: 17
Query Match: 58.73% Indels: 12
DB: 13 Gaps: 1

US-09-367-052-2 (1-359) x B1756157 (1-875)

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QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
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Db 129 ATGAAGGAACCCGTGTTCCGTGAAGAAATGCTAATTCATTAATAATCTTCCTGCCAC 188
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Db 249 GGTTCACGAAAGAAAGAACTGAGAGCATGACGAGCAAGTACAGGCTCAGCTGAGTGC 308
QY 86 AspleuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTyrPyr 105
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QY	126	ValLeuLeuLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn	145
Db	429	GTCTCATCTCCGTGCTTCATCAGTCTGACCGCATCCGCGCATTCGTCACGCACACAC	488
QY	146	SerGlnArgProArgLysLeuLeuAlaGluLysAlaValAlaTyrValGlyValTrpIlePro	165
Db	489	AGTCAGAGGCCAGAGAGACGTGTGGCTGTAAGAAGTGCTATGTTGGGCTTGATCCCT	548
QY	166	AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer	185
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QY	205	IlePheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys	225
Db	654	GTC-CAGTTTCAGACATCATGTTGGCTTATCTGCTGGTATGTCATCTGCTCTG	712
QY	225	STyrCysIle-IleIleSerLysLeuSer-HisSer-LysGlyHisGlnLysArgLysAla	244
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Db	773	-CTCAGGAACACAGTCATCTCATCTCTGGGTTTCTTCCCTGAGTGGCTTACTACAT	831
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RESULT 9
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 B1754094
 version
 B1754094.1
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 EST.
 source
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 organism
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 905)
 NIH-MGC <http://mgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 tissue procurement: Life Technologies, Inc.
 cDNA library preparation: Life Technologies, Inc.
 cDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Incyte Genomics, Inc.
 clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 plate: L14M11495 row: f column: 13
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 Location/Qualifiers

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1. .905
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Site: 2; EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
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primed and directionally cloned (ccory site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gubert (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH-MGC Library."

Alignment Scores:	
Pred. No.:	2,37e-124
Score:	1093.50
Percent Similarity:	89.47%
Best Local Similarity:	83.51%
Query Match:	58.57%
DB:	13
	Length: 905
	Matches: 238
	Conservative: 17
	Mismatches: 13
	Indels: 3
	Gaps: 3

QY	6	valserlleIeYrThSerAspaSnIySerGIuGIuValGIySerGIySPrIyAspSer	25
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Db	376	TTTGGGAACTTCTCTATGCAAGCAGCATGTCATCATACAGTCAACCTCTACACAGT	435
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Db	436	GTCCATCATCTCGCCCTTCATCAGCTGGAGCCCTACCTGGCATCGTCCACGGCACAC	495
QY	146	SerGIuArgProArgLySLeuLeuAlaGlyLysAlaValIyTrValGIyAlTrpIIlePro	165
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QY	243	salalaLeuLyStrhTrhValIIleLeuIIleLeuAlaPhePheAlaCysTrpLeuProYrTy	263
Db	781	GC--CTCAAGACACAGTATCCTCATCCCTGCTTCTTCGCTGTGGGG--CCTTACTCA	837
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 ACCESSION BM387369
 VERSION BM387369.1 GI:18187422
 SOURCE EST.
 ORGANISM Norway rat.
 Rattus norvegicus
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 765)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 9704447
 Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to identify it as a clone from the
 normalized cervix library cDNA Library Preparation: M.B. Soares Lab
 Clone distribution: clones will be available through Research
 Genetics (www.resgen.com)
 Seq primer: M13 Forward
 PolA-Tes.

FEATURES Source

1. 765
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 polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-CNI
 library is a subcloned library derived from the following
 pool of seven normalized rat libraries: normalized rat
 seminal vesicles, normalized rat penis, normalized rat
 bladder, normalized rat cervix, normalized rat brown
 adipose, normalized rat fundus, and normalized rat
 salivary gland. It was constructed according to the
 procedure described by Bonaldo, Lennon & Soares (Genome
 Research genome 6: 791-806, 1996). For construction of
 the CNI library, plasmid DNA from the pool of normalized
 libraries was electroporated into competent bacteria for
 the production of single-stranded circular DNA. This was
 then used as a tracer in a subtractive hybridization with
 a driver (PCR amplified inserts from a plasmid DNA template
 preparation) comprising: a) a pool of about 34,000 clones
 from the Rat Unigene Set corresponding to plates R-5-AA-NN
 excluding plates R-5-MM and MN. This pool represented 40%
 of the final driver population. b) a pool of about 29,000
 clones from subtracted libraries CA0 and CA1 corresponding
 to plates R-CA0-AMV through R-CA0-AXS, R-CA0-AXZ through
 R-CA0-BAZ, R-CA0-BFE through R-CA0-BHY, R-CA0-BJS,

R-CA0-BKE, R-CA0-BKG-H, R-CA0-BKJ-K, R-CA0-BKP through
 R-CA0-BKS, R-CA0-BKU-V, R-CA0-BLY through R-CA0-BMA,
 R-CA0-BMC through R-CA0-BME, R-CA0-BNS, R-CA0-BOB through
 R-CA0-BOJ, R-CA0-BPA through R-CA0-BRG, R-CA1-BBA through
 R-CA1-BDA, R-CA1-BHJ through R-CA1-BJF, R-CA1-BJR,
 R-CA1-BJT through R-CA1-BKB, R-CA1-BKD, R-CA1-BKI,
 R-CA1-BKT, R-CA1-BKT, R-CA1-BLE, R-CA1-BLH through
 R-CA1-BLN, R-CA1-BLS, R-CA1-BLV-V, R-CA1-BNR, and
 R-CA1-BLE. The resulting pool represented 20% of the
 final driver population. c) a pool of about 15,000 clones
 from non-normalized libraries CS0s, CT0s, CU0s, CW0s, CX0s
 and normalized libraries CS0, CT0, CU0, CW0, and CX0
 corresponding to plates R-CS0s-CBP through R-CS0s-CBO,
 R-CT0s-CAM through R-CT0s-CAX, R-CU0s-CBP through
 R-CU0s-CCA, R-CW0s-CCB through R-CW0s-CCM, R-CX0s-CCN
 through R-CX0s-CCX, R-CS0-BSD, R-CS0-BTD through R-CS0-BTV
 R-CS0-BWV, R-CT0-BTW through R-CT0-BUP, R-CT0-BVN,
 R-CU0-BUQ through R-CU0-BVL, R-CW0-BVY through R-CW0-BWP,
 R-CW0-BXN through R-CW0-BXO, R-CX0-BWQ through R-CX0-BXM.
 The resulting pool represented 5% of the final driver
 population. d) a pool of about 5,000 clones (1,000 from
 non-normalized eye library CV0 and 4,000 from normalized
 eye library CV1) corresponding to plates R-CV0-BRH through
 R-CV0-BRR, R-CV1-BRS through R-CV1-BSC, R-CV1-BSE through
 R-CV1-BTC, and R-CV1-BVO through R-CV1-BVU. This pool
 represented about 5% of the final driver population. e) A
 pool of about 10,000 clones from subtracted library BS2,
 BV0 and BV0P (7.9.5 kb cDNA library fraction from rat
 whole embryo), and BX0 (0.5.7kb cDNA library fraction from
 rat whole embryo) corresponding to plates R-BS2-BDB
 through R-BS2-BFB, R-BV0-ANR through R-BV0-ANR, R-BV0P-AOI
 through R-BV0P-AOX, and R-BX0-AOY through R-BX0-ASH. The
 resulting pool represented 5% of the final driver
 population. f) a pool of about 7,000 clones from the
 seven non-normalized libraries that make up the tracer
 including CY0, CZ0, DA0, DB0, DC0, DD0, and DE0
 corresponding to plates R-CY0-BXP through R-CY0-BXZ,
 R-CZ0-BYA through R-CZ0-BYL, R-CZ0-BXB-C, R-DA0-BXJ
 through R-DA0-BYP, R-DA0-BBD through R-DA0-BZH, R-DB0-BYO
 through R-DB0-BZA, R-DC0-BZI through R-DC0-BZQ, R-DD0-CAY
 through R-DD0-CBA, R-DD0-BER through R-DD0-CAI,
 R-DD0-CBB-C, and R-DE0-CAB through R-DE0-CAL. The
 resulting pool represented about 10% of the final driver
 population. g) a pool of about 2,000 clones from the pool
 of normalized libraries, CN0, that makes up the tracer.
 The corresponding plates are R-CN0-BKW through R-CN0-BLD,
 R-CN0-BLG, R-CN0-BLP through R-CN0-BLR, R-CN0-BLT,
 R-CN0-BMW-X, R-CN0-BMB, and R-CN0-BMF through R-CN0-BML.
 This pool represented 5% of the final driver population.
 h) a pool of the 28 most abundant clones in the CN0 pool
 corresponding to the following addresses: bkx-a-09-0-UI,
 bkx-b-09-0-UI, bkx-b-11-0-UI, bkx-b-10-0-UI, bkx-d-01-0-UI,
 bkx-d-06-0-UI, bkx-g-08-0-UI, bkx-h-12-0-UI,
 bkx-a-05-0-UI, bkz-a-06-0-UI, bkz-a-11-0-UI, bkz-c-06-0-UI,
 bkz-c-09-0-UI, bkz-d-10-0-UI, bla-a-01-0-UI,
 bla-a-02-0-UI, bla-f-04-0-UI, bla-g-07-0-UI, bla-g-12-0-UI,
 blb-a-12-0-UI, blb-f-02-0-UI, blc-a-11-0-UI,
 blc-e-95-0-UI, bld-1-08-0-UI, bld-f-02-0-UI, blq-h-04-0-UI,
 blr-a-05-0-UI, blt-f-08-0-UI. This pool represented 5%
 of the final driver population. i) One abundant CN0 clone
 (corresponding to the address bkz-a-11-0-UI) was digested
 with NotI and Eco RI and the resulting insert was gel
 purified. This purified insert was added directly to the
 driver so that it represented 5% of the final driver
 population.

BASE COUNT 157 a 211 c 194 g 202 t 1 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.33e-123 Length: 765

Score: 1086.50 Matches: 212
 Percent Similarity: 94.71% Conservative: 3
 Best Local Similarity: 93.39% Mismatches: 7
 Query Match: 58.19% Indels: 5
 DB: 13 Gaps: 1

US-09-367-052-2 (1-359) x BM387369 (1-765)

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QY 4 ILESERVALSERILEYTHRRSERASPSANTYRSERGLNGLVALGLYSERGLYASPTYR 23
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QY 24 ASPSERANLYSGIUPROCYSPHEARASPGIUNASVALHISPHESANARGILEPHELEU 43
DB 158 GACGCCAACAAGAAACCTCGCTCCGGAGTGAAGAAACCAACTCAACAGAGATCTCTG 217
QY 44 PROTHRIETRYRPHIELLEIIPHELEUTHRIEVALGLYSANGLYLEUVALILELEU 63
DB 218 CCCAGCATATATTTATATCTTCTGACGCGATGAGGCAATGGGTTGGTAAATCTG 277
QY 64 VALMETGLYTRGILNLSYLSLEUARGSERMETHRASPSTYRATRYRGLNGLHISLEUSER 83
DB 278 GTCTAGGCTTACAGAAAGAGCTGAGAGCATGACAGACAAGTACCGGCTGCACCTTCC 337
QY 84 VALALASPHEULEUPHEVALILETHRIEUPROPHETRPALAVALAASPALAMETALAASP 103
DB 338 GTGGCTACCTCCCTTGTGATCAGACTCCCTCTGGGACAGTGGACGCCATGGCTGAC 397
QY 104 TRPTIYRPHIEGLYSPHELEUCYLSVALAVALHISLEILEYTHRVALASNLTYR 123
DB 398 TGGTACTTTGGAAATTTATGTAAGCTGTGATCATCATACACCGTCAACCTTTAC 457
QY 124 SERSERVALLEULEUVALIAPHIELLESERLEUSAPARGTRYRLEUVALILEVALHISALA 143
DB 458 AGCAGTTCCTCATCTCGCCCTTCATACGCTGAGACGCTTCCATCTTCCATCTCCACGCC 517
QY 144 THRASNSEGLNARGPROARGLYSLEULEUVALAGLULYSALAVATRYVALGLYVALTRP 163
DB 518 ACCAAGACGACGAGCGGAGAGAGCTGTGGCTGAAGAGCCGCTCATGTGGGCTGTGG 577
QY 164 ILEPROALALEULEUTHRIEPROASPHEILEPHEALASPVALSERGLNGLYASP 183
DB 578 ATCCCCCCTCCCTCCGACTATCCGACATCATCTTCCCGATGTC----- 625
QY 184 ILESERGLNGLYASPARGTRYRILECYASPARGTRYRPROASPSERLEUTRIMET 203
DB 626 ---AGCCAGGGGAGCGGACGATCATCTGTACCGCTTTACCCGACAGCTGTGGATG 682
QY 204 VALVALPHEGLNPHIEGLNGLHISMETVALGLYDEULEUPROGLYILEVALILELEU 223
DB 683 GTGGTGTTCAGTTCACGACATCATGTGGTCTCATCCCTGGGGCATGCTCATCTCTG 742
QY 224 SERCYSTRYRYSILEILEIE 230
DB 743 TCCGTGACTGCATCATCATC 763

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RESULT 11
 .BG613352 750 bp mRNA linear EST 18-APR-2001
 LOCUS 602641234F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4772288 5',
 DEFINITION
 ACCESSION BG613352
 VERSION BG613352.1 GI:13664723
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: c9apbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LICM642 row: c column: 09
 High quality sequence stop: 726.
 Location/Qualifiers

FEATURES

source

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1. 750
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/clone="IMAGE:4772288"
/clone_1ib="NIH_MGC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:  

SfiI (ggcgctcgcc); Site_2: SfiI (ggccatgatgc);  

Double-stranded cDNA was prepared from cell line RNA. 5'  

and 3' adaptors were used in cloning as follows: 5'  

sequence: 5'-ATTCTAGAGCCGAGCGGCCGACATG-dT(30)BN-3'  

(where B = A, C, or G and N = A, C, G, or T). Average  

insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies  

contained inserts by PCR. This library was enriched for  

full-length clones and was constructed by Clontech  

Laboratories (Palo Alto, CA). Note: This is a NIH-MGC  

Library."

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BASE COUNT

165 a 219 c 166 g 200 t

ORIGIN

Alignment Scores:

Pred. No.: 4.04e-123 Length: 750
 Score: 1082.50 Matches: 220
 Percent Similarity: 91.41% Conservative: 14
 Best Local Similarity: 85.94% Mismatches: 14
 Query Match: 57.98% Indels: 9
 DB: 12 Gaps: 1

US-09-367-052-2 (1-359) x BG613352 (1-750)

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QY 33 ASPLUNASVALHISPHESANARGILEPHELEUPROTHRIETRYRPHIELLEPHELEU 52
DB 1 GAAGAAATGCTATATTTCATTAATCTTCCTGCCACCATCTACATCATCTTCTTA 60
QY 53 THRGLYILEVALGLYSANGLYLEUVALILELEUVALMETGLYTRGILNLSYLSLEUARG 72
DB 61 ACTGTCATGTGGGCAATGATGATGTCATCTGTCATGAGTTAACGAAAGATGAGA 120
QY 73 SERMETHRASPSTYRATRYRGLNGLHISLEUSERVALALASPHEULEUPHEVALILETHR 92
DB 121 AGCATGACGACAGAAAGTACAGCTGTCACGTGTCAGTCCCTCTTGTGCATCAGC 180
QY 93 LEUPROPHETRPALAVALAASPALAMETALAASPTRYRPHIEGLYSPHELEUCYLS 112
DB 181 CTTCCTTCCTGGGACAGTGTGATGCTGGGCAACTGTGACTTTGGAACTTCATGCAAG 240
QY 113 ALAVAHISLEILEYTHRTRVALASNLTYRSESERVALLEULEUVALIAPHIEIE 132
DB 241 GCAGTCATCATCATCATACAGTCAACCTCTACAGAGTCTCTCATCTCGGCTTCATC 300
QY 133 SERLEUSAPARGTRYRLEUALIIEVALHISALATHRASNSEGLNARGPROARGLYSLEU 152
DB 301 AGCTGACCGCTACCTGCGCATGTCACAGCCACCAAGTCAAGAGCCCAAGAGCTG 360
QY 153 LEUVALGLNLSYLSVALYTRYVALGLYVALTRPILIEPROALALEUUTHRIEPRO 172
DB 361 TTGGCTGAAGAGTGTCTATGTGGGCTGTGATCCCTCCCTCTGCACTATTTCC 420
QY 173 ASPPHEILEPHEALASPVALSERGLNGLYASPILESERGLNGLYASPARGTRYRILE 192
DB 173 ASPPHEILEPHEALASPVALSERGLNGLYASPILESERGLNGLYASPARGTRYRILE 192

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Oy		98	ValsaplaImetAlaAsprTPYrPhBgILysSheucysLysValaHisIle	117
Db		122	GTTGATCCCGTGGCAAACTGTACT--GGGAACCTCTATGCAGGACATCATC	180
Oy		118	TyrThrValAsnLeuTySerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyr	137
Oy		181	TACACACTCAACCTCTACAGCAGGTCTTCATCTTGCGCTTCATCATCTGGACCGCTAC	240
Db		138	LeuAlaIleValHisAlaThrAsnSerGlnArgProArgLysLeuAlaGluValA	157
Oy		241	CTGGCCATCGGCCACGCCAACAGTCAGGCGCAAGAAGCTGTGGCTGGAAAAGGTG	300
Db		158	ValTyrrValGlyValTrpIleProAlaLeuLeuLeuThrIleProAspPheIlePheAla	177
Oy		301	GTCATATGTGGCGCTGTGGATCCCTGCCCTCTGTAATATCCGACTTCATCTTGCC	360
Db		178	AspValSerGlnGlyAspIleSerGlnGlyAspAspArgTyrIleCysAspArgLeuTyr	197
Oy		361	AACCTG-----AGGAGCGACATACAGATAATATCTGTGACCCTTCTAC	405
Db		198	ProAspSerLeuTrpMetValValaPheGlnPheGlnHisIleMetValGlyLeuIleLeu	217
Oy		406	CCCAATAGACTGTGGTGCGTTGTCTTCACAGTTTACGACATCATGTGGCGCTATCTCG	465
Db		218	ProGlyIleValIleLeuSerCysTyrCysIleIleIleSerLysLeuSerHisSerLys	237
Oy		466	CCTGGATTGTGCATCCCTGCTCTGATTTGATTCATTCACAAGCTGCACATCCCAAG	525
Db		238	GlyHisGlnLysArgLysAlaLeuLysThrThraIleLeuIleLeuAlaIlePheAla	257
Oy		526	GGCCACCAAGAGGCCAAGCCCTCAGAACCAACATCCATCTCGGGCTTTCTTGCC	585
Db		258	CysTrpLeuProTyrTyrValGlyIleSerIleAspSerPheIleLeuLeu-GlyValI	277
Oy		586	TGTTGGCTGCT-FACTACAT-GGGATCAGCATGACTCTTCATCTCGTGGGAATCAT	643
Db		277	eLygInGlnGlyCysAspPheGlnSerIleValHisLysTrpIleSerIleThrGluAla	297
Oy		644	CMAACAGCGTGTGATTGACGAAACATCGTGCCCAAGGGGATTCATTCACCGAGGCGCTA	703
Db		297	uaIaPhePheHisCysCysLeuAsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLys	317
Oy		704	AGTTTCTCTCCACATCGGTGTGAACCCAAACTGT---AGCTTCTT-GGAACAATAITAA	759
Db		317	sSerSerAlaGlnHisAlaLeuAsnSerMetSerArgGlySerSerLeuLysIleLeuSe	337
Oy		760	CTCTGGCCAGACGACATCACTCGGGAGCA-----GAGGTCCAGATC	798
Db		337	Lys--GlyLysArgGlyGlyHisSerSerVal	347
Oy		799	AAAGACTTCCAAGAGAGGGGCGCATCACGCT	832
Db				
RESULT 15				
BIS97875				
LOCUS		742 bp	mRNA	linear EST 07-SEP-2001
DEFINITION		603245357F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5287575 5',		
ACCESSION			mRNA sequence.	
VERSION		BIS97875		
KEYWORDS		BIS97875.1 GI:15490814		
SOURCE		EST.		
ORGANISM		human.		
		Homo sapiens		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE		1 (bases 1 to 742)		
AUTHORS		NIH-MGC http://mgc.nci.nih.gov/.		
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL		Unpublished (1999)		
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov Tissue Procurement: MIKLOS Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki Toshiyuki and Piero Carninci (RIKEN)		

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FEATURES
source
    cdna Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LNL at:
    http://image.lnl.gov
    Plate: L1AM1727 row: a column: 16
    High quality sequence stop: 739.
    Location/Qualifiers
        1..742

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/clone="IMAGE:5287575"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pBluescriptpr (modified
pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcgag
); Oligo-dt primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.3 kb and
normalized to R0T 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NIHGR1, National
Institutes of Health). Note: this is a NIH-MGC Library."

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Alignment Scores:	
Pred. NO.:	2,299-110
Score:	979.50
Percent Similarity:	93.15%
Best Local Similarity:	87.21%
Query Match:	52.46%
DB:	13
Length:	742
Matches:	191
Conservative:	13
Mismatches:	7
Indels:	
Gaps:	1

US-09-367-052-2 (1-359) x BI597875 (1-742)

QY	6	ValserIleThrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer	25
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Db	103	ATCAGTATATACACTTCAGATACACTACCCAGGAAATGGGCTCAGGGGACTATGACTCC	162
QY	26	AsnIysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr	45
		::	
Db	163	ATGAGGAGCAACCCGTTCCTCCGGAAGAAATCTCAATTCAATTAATCTTCCTGCCACC	222
QY	46	IleIleThrIleIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet	65
Db	223	ATTCATCTCCATCAATCTCTTAACGTGGCATTTGTGGCAATGGATGGTATCTTGCTGTG	282
QY	66	GlyTyrGlnIysLysLeuArgSerMetThrAspTyrTyrArgLeuHisLeuSerValAla	85
Db	283	GGTTACCGAGAAACTAGAGAGCATAGCGGACACAGTACAGCTGCACCTTCACGTGCC	342
QY	86	AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr	105
		::	
Db	343	GACCTCCTCTTTGCATCACCCCTCCCTTCGGGCGAGTTGATGCCGTGGCAACGTGATAC	402
QY	106	PheGlyLysPheLeuCysLysAlaValHisIleIleTyrTrpValAsnLeuTyrSerSer	125
		::	
Db	403	TTTGGGAACCTCCATACGAGGAGGTCCATCTATCTACACAGTCAACCTTACAGCAGT	462
QY	126	ValIleuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisIleThrAsn	145
		::	
Db	463	GTCCTCATCCCGGGCCTTCATAGTCTGGACCGCTACCTGGCCATCGTCCAGCCACCAC	522
QY	146	SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro	165
		::	
Db	523	AGTCAGAGAGCCAAAGGAAGCTGTGGCTGGAAGAGTGCTGTATGTTGGCGCTGTGATCCCT	582
QY	166	AlaIleuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer	185
		::	
Db	583	GGCTCTCCGCTGACATATTCGCCAGCTTCACTCTTGGCCACGTC-----AGT	627

Oy 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyr-MetValIva 205
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 Db 628 GAGGAGATGACAGATATATCTGTGACCGCTTCTACCCCATGACTGTGGTGTGTGT 687
 Oy 205 IPhcGln-PheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIle 222
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 Db 688 GTCCCAAGTTTCAGCACATCATGGTGGCTTATTCGCTGATGTGTCATC 740

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